



10724598
SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: BLANCHE, FRANCIS; CAMERON, BEATRICE; CROUZET, JOEL; DEBUSSCHE, LAURENT; LEVCY SCHIL, SOPHIE; THIBAUT, DENIS
- (ii) TITLE OF INVENTION: POLYPEPTIDES INVOLVED IN THE BIOSYNTHESIS OF COBALAMINS AND/OR COBAMIDES, DNA SEQUENCES CODING FOR THESE POLYPEPTIDES, PREPARATION METHOD AND THEIR USE.
- (iii) NUMBER OF SEQUENCES: 60
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER
 - (B) STREET: 1300 I STREET, N.W.
 - (C) CITY: WASHINGTON
 - (D) STATE: DISTRICT OF COLUMBIA
 - (E) COUNTRY: USA
 - (F) ZIP: 20005
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: FLOPPY DISK
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WORDPERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 10/724,598
 - (B) FILING DATE: 01-DEC-2003
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/426,630
 - (B) FILING DATE: 21-APR-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/916,151
 - (B) FILING DATE: 14-SEP-1992
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/FR91/00054
 - (B) FILING DATE: 30-JAN-1991
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: S.J. ARRIGO
 - (B) REGISTRATION NUMBER: 46,063
 - (C) REFERENCE/DOCKET NUMBER: 03806.0050-02000
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202) 408-4160
 - (B) TELEFAX: (202) 408-4400

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5398 base pairs
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(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas denitrificans*
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Nucleotide sequence of the 5' to 3' strand from the 5398 bp *Cla*I-HindIII-HindIII-HindIII fragment of *Pseudomonas denitrificans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGGCTGCAGG	TCGACTCTAG	AATCGATGAA	GCCTGCGATG	AAGGCGGCGA	CGAACAGGAA	60
GGCGAGCAGG	TGGAAGGCGA	GATCTTGCAC	GGCGGGGACT	CGAGAGGAGA	GCTGTCAGGC	120
GGGATTTTCC	GCCTTGTGTC	AGAGCCCGGC	GCGATTTGCA	AAGCCTTCTG	TCGCGGTGTT	180
GCTGTCCATG	CAGGTGTCGA	AATTGAAAAA	CCGACAAAGA	TTCACAGCCT	TGTTCCAGCT	240
CGCTGTCTTT	CTGGATGGAG	GCGCTCTCGC	CCGCATGGTG	CCGAAGAAGG	GCTGTCCTTG	300
CGATACGGTA	GGCGGATGAC	GATCTTCCTC	AAACGCGACA	TGGCGATGGC	GCAATCCGGT	360
TTGACCGGCC	TTCCGCGCTC	CGGTAAAAAT	GAAGGATATG	CGACGGCGTC	CGCTTTGGCG	420
GACTGAAAGA	GCGTCCGGTG	CGGCCGACCC	AGTCAGGGGG	GCATCAGCCG	GTGCTGTCCA	480
GATCGGCCGG	GACGGATCGT	CCCAGCCGGC	GCTTCGTTAA	GGAGAACAAC	GAAGGGAGCC	540
GGCCGCCGAT	GCCATCGGGC	CAACACTCTG	CACAGACGAC	GAAAGCAGGA	GCCGGGCTGG	600
TGCTCGGGCT	CGGCTGCGAG	CGTCGCACGC	CGGCCGAAGA	GGTGATCGCC	CTTGCCGAGC	660
GTGCGCTTGC	CGATGCCGGT	GTTGCGCCCC	GCGATCTGCG	GCTGGTCGCC	TCGCTCGATG	720
CTCGCGCCGA	GGAGCCGGCG	ATCCTGGCGG	CCGCTCAGCA	TTTCGCGGTT	CCGGCCGCGT	780
TCTACGATGC	CGCCACGCTC	GAAGCCGAAG	CTTCCC GGCT	CGCCAACCCG	TCCGAGATCG	840
TCTTTGCCTA	CACGGGTTGT	CATGGCGTTG	CGAGGGTGTC	AGCGCTCGTC	GGCGCCGGTC	900
GCGAAGCCGT	GCTGATTGTG	CAGAAGATCG	TCTCCGCCCA	TGCGACGGCC	GCACTTGCCG	960
GGCCGGCGAC	CTTGCGCGCC	GAAAAGCGCA	TCCAGGCGGC	GGAGGCTGTC	TGATGCATTC	1020
TTATGTTGTT	GAATTGAATC	AATCTTTTGC	CCGGGGTTTC	TCTCAAGTGG	AATCCGGTTC	1080
TTTAGAGAGC	GCGTCAGGCG	TGCCGTTGGG	TGGCGCCGAA	ATACAGGTGG	GACAGCACGC	1140
ATGATCGAGC	ACCTCTTTGC	CGGATTGCCG	GCGCTCGAAA	AAGGTTTCGGT	CTGGCTGGTC	1200
GGCGCCGGCC	CCGGCGATCC	CGGCCTGTTG	ACGCTGCATG	CGGCCAATGC	GCTGCGCCAG	1260
GCGGATGTGA	TCGTGCATGA	TGCGCTGGTC	AACGAGGATT	GCCTGAAGCT	CGCGCGGCCG	1320
GGCGCCGTGC	TGGAGTTTGC	GGGCAAGCGT	GGCGGCAAGC	CGTCGCCGAA	GCAGCGCGAC	1380
ATCTCGCTTC	GCCTCGTCGA	ACTCGCGCGC	GCCGGCAACC	GGGTGCTGCG	CCTCAAAGGC	1440
GGCGATCCCT	TCGTCTTCGG	TCGCGGTGGC	GAGGAGGCGC	TGACGCTGGT	CGAACACCAG	1500
GTGCCGTTCC	GAATCGTGCC	CGGCATCACC	GCCGGTATCG	GCGGGCTTGC	CTATGCCGGC	1560
ATTCCCGTGA	CCCATCGCGA	GGTCAACCAC	CGGGTCACTT	TCCTGACTGG	CCATGATTCC	1620
TCCGGCCTGG	TGCCGGATCG	CATCAACTGG	CAGGGCATCG	CCAGCGGCTC	GCCTGTCATC	1680
GTCATGTACA	TGGCGATGAA	ACATATCGGC	GCGATCACCG	CCAACCTCAT	TGCCGGCGGC	1740
CGCTCGCCGG	ACGAACCGGT	CGCCTTCGTC	TGCAACGCCG	CGACGCCGCA	GCAGGCGGTG	1800
CTGGAAACGA	CGCTTGCGCG	TGCAGAGGCC	GATGTTGCGG	CGGCAGGGCT	GGAGCCGCCG	1860
GCGATCCGTC	TCGTGCGCGA	GGTGGTGCGG	CTCGCGCAG	GCTCGGCTG	GATCGGCGCG	1920
CTGACGGGGC	GCAAGCTTGC	CGCCGACCCG	TTCGCCAATC	GCATTCTCAG	GAACCCGGCA	1980

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TGAGCGGATT	GCTGATTGCC	GCACCCGCGT	CCGGCTCCGG	CAAGACGACG	GTGACGCTCG	2040
GGCTGATGCG	CGCCCTGAAG	AGGCGCGGCG	TGGCGATCGC	GCCC GGCAAG	GCGGGGCCGG	2100
ACTATATCGA	TCCCCGTTTC	CACGCGGCAG	CGACCGGCGA	GCCCTGCTTC	AACTACGACC	2160
CCTGGGCGAT	GCGCCCGGAA	CTGCTGCTTG	CCAATGCGTC	GCATGTGGCC	TCCGGCGGGC	2220
GCACATTGAT	CGTCGAGGCG	ATGATGGGAC	TGCATGACGG	TGCTGCCGAC	GGCTCGGGAA	2280
CGCCAGCGGA	CCTCGCCGCG	ACGCTGAACC	TTGCGGTCAT	TCTGGTGGTC	GATTGCGCCC	2340
GCATGTCCCA	GTCGGTTGCC	GCCCTCGTGC	GCGGCTATCG	GGATCATCGC	GACGATATCC	2400
GGGTGGTTGG	CGTCATCCTC	AACAAGGTCG	GCAGCGATCG	GCATGAAATG	ATGCTGCGCG	2460
ATGCGCTCGG	CAAGGTGCGC	ATGCCTGTCT	TCGGCGTGCT	CCGGCAGGAC	AGCGCATTGC	2520
AACTGCCGGA	GCGCCATCTC	GGGCTCGTGC	AGGCGGGCGA	ACACTCAGCG	CTTGAGGGCT	2580
TCATCGAGGC	GGCGGCCGCG	CGGGTCGAGG	CTGCCTGCGA	TCTCGACGCC	ATCCGCCTGA	2640
TCGCGACGAT	TTTCCCCGAG	GTGCCCCGCG	CGGCCGATGC	CGAGCGTTTG	CGGCCGCTCG	2700
GTCAGCGCAT	CGCGGTCGCG	CGCGATATCG	CCTTTGCCTT	CTGCTACGAG	CACCTGCTTT	2760
ACGGCTGGCG	GCGAGGCGCG	GCGGAGATTT	CCTTCTTCTC	GCCGCTCGCC	GACGAGGGGC	2820
CGGATGCGGC	AGCCGATGCC	GTCTATCTTC	CGGGGGTTA	TCCGGAGCTG	CATGCGGGGC	2880
AGCTGAGCGC	CGCCGCCCGA	TTCCGTTCCG	GCATGCATTC	CGCGGCGGAA	CGCGGCGCCC	2940
GCATCTTCGG	CGAGTGCGGC	GGCTATATGG	TGCTCGGCGA	AGGGCTTGTC	GCTGCCGATG	3000
GCACACGCTA	CGACATGCTC	GGCCTGCTGC	CGCTCGTAAC	CAGTTTTGCC	GAGCGCAGGC	3060
GGCACCTCGG	CTATCGCCCG	GTGCTGCCTG	TCGACAACGC	CTTCTTCGAT	GGACCCATGA	3120
CGGCGCACGA	ATTCCACTAT	GCGACCATCG	TGCGCGAAGG	GGCGGCCGAT	CGGCTGTTTG	3180
CGGTGAGCGA	CGCCGCGGCG	GAGGATCTCG	GCCAGGCGGG	CCTCCGGCGC	GGCCCTGTCG	3240
CCGGTTCCTT	CATGCATCTG	ATCGACGTCG	CAGGTGCTGC	ATGAGCGCAC	CGATCGTTCA	3300
TGGTGGCGGC	ATCACCGAGG	CCGACGCGCG	CTATGGCGGC	CGGCCTGAAG	ACTGGCTCGA	3360
TCTGTGACCC	GGCATCAATC	CATGCCCCGT	CGCCTTGCCC	GCGGTCCCTG	AGCGCGCCTG	3420
GCACCGGCTG	CCGGATCGCG	AGACGGTAGA	TGATGCGCGG	AGCGCCGCCG	CCGACTACTA	3480
CCGCACCAAC	GGCGTGCTGC	CTTTGCCGGT	GCCGGGCACC	CAGTCGGTGA	TCCAGCTCCT	3540
GCCACGTCTT	GCTCCGGCCA	ACAGGCACGT	CGCGATTTTC	GGGCCGACCT	ATGGCGAGTA	3600
TGCCCCGCGT	CTTGAAGCGG	CCGGCTTTGC	TGTCGATCGC	GTGCGGGATG	CCGACGCGCT	3660
CACGGCCGAA	CATGGGCTTG	TCATCGTCGT	CAACCCCAAC	AACCCGACCG	GCCGCGCCTT	3720
GGCGCCGGCG	GAGCTTCTGG	CGATCGCCGC	AAGGCAGAAG	GCGAGCGGCG	GACTGCTGCT	3780
GGTCGATGAG	GCCTTCGGCG	ATCTTGAGCC	GCAACTGAGT	GTGCTGGTTC	ACGCGTCAGG	3840
GCAAGGCAAC	CTCATCGTCT	TCCGCTCCTT	CGGCAAGTTC	TTCCGCTTGG	CGGGCCTGCG	3900
CCTCGGCTTC	GTCGTTGCGA	CCGAGCCAGT	GCTTGATCC	TTTGCCGATT	GGCTCGGTCC	3960
CTGGGCTGTC	TCCGGCCCCG	CGTTGACGAT	CTCGAAAGCG	CTGATGCAGG	GCGATACGAA	4020
GGCGATCGCG	GCGGGCATCC	TCGAGCGTCG	CGCCGGCCTC	GATGCGGCTC	TCGATGGGGC	4080
AGGGCTCAAC	CGTATCGGCG	GCACGGGGCT	ATTCTGTCTG	GTGAGCATC	CCAGGGCAGC	4140
TCTGCTGCAG	GAGCGGCTCT	GCGAGGCCCA	TATTCTCACG	CGCAAGTTTC	ACTATGCCCC	4200
GACCTGGCTC	AGGGTCGGT	TTGCGCTGAG	CGCGGCTGGT	GACCGACGGC	TGGCGGACGC	4260
GCTTGCCCGC	ATGGAGCTCT	GAGGTGTCGG	AGACGATCCT	GCTCATTCTC	GCGCTGGCGC	4320
TGGTGATCGA	CCGCGTTGTC	GGCGATCCGG	ACTGGCTCTG	GGCGCGCGTG	CCGCATCCGG	4380
TCGTGTTTTT	CGGCAAGGCC	ATCGGCTTTT	TCGACGCGCG	GCTGAACCGG	GAGGACCTCG	4440
AGGATAGCGC	GCGCAAATTT	CGTGGCGTCG	TCGCGATCCT	TTTGTTGCTT	GGCATCAGCG	4500
CCTGGTTCGG	CCATCTGCTG	CATCGCCTGT	TCGCCGTGCT	CGGACCGCTC	GGCTTTCTGC	4560
TCGAGGCGGT	TCTGGTCGCG	GTCTTCTGG	CACAGAAGAG	CCTCGCCGAT	CACGTGCGTC	4620
GCGTGCCCGG	GGGCTTGCGA	CAGGGCGGGC	TGGAAGGCGG	GCGTGCCGCC	GTGTCGATGA	4680
TCGTTGGTCG	CGATCCAAAG	ACGCTCGACG	AGCCGGCGGT	CTGCCGTGCC	GCGATCGAAA	4740
GCCTTGCCGA	GAATTTCTCC	GACGGCGTCG	TGGCGCCGGC	CTTCTGGTAC	GCGGTTGCCG	4800
GCCTGCCGGG	GCTTCTTGCC	TACAAGATGC	TGAACACCGC	CGATTCGATG	ATCGGCCACA	4860
AGTCGCCGAA	ATATCTGCAC	TTCCGGCTGG	CCTCGGCCCG	ACTCGACGAT	CTCGCCAACC	4920
TGCCGGCAGC	GAGGCTCTCG	ATCCTTTTGA	TCTCAGCCGG	TGCGCTGATC	CATCGTGGCG	4980
CCAGCGCCGC	CAAGGATGCG	CTGACCGTGG	CCCTTCGCGA	CCATGGCCTG	CACCGCTCGC	5040
CGAACTCCGG	CTGGCCGGAA	GCGGCCATGG	CCGGCGCGCT	CGATCTGCAG	CTTGCCGGTC	5100
CGCGGATCTA	TGGCGGCGTC	AAGGTCAGCG	AACCTATGAT	CAACGGTCCG	GGCCGAGCGG	5160
TTGCAACAAG	CGAAGACATC	GACGCCGGTA	TTGCTGTATT	TTATGGCGCC	TGTACGGTCA	5220
TGGCCGGGTT	TGTTCTTGCA	ATCGCAATGA	TTTGATCGCG	GAAGTTGACC	TTGCGATTAA	5280
GACTCTGCTT	TCCATATGTA	TTAAGATCGT	ATCATATTTC	ATCAGTTATT	CTCCTGGAAC	5340
GTTTGGTTCC	ACCGGTACGT	GTTCGTCTTC	CCGGAGAGAG	AAGCATGCGC	AAAAGCTT	5398

(2) INFORMATION FOR SEQ ID NO: 2:

(i)

SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8753 base pairs

(B) TYPE: Nucleic Acid

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(C) STRANDEDNESS: Double
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas denitrificans*
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Nucleotide Sequence of the 5' to 3' strand from the 8753 bp EcoRII fragment of *Pseudomonas denitrificans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GAATTCGCCA	GCGCCTACAT	GGCTGACCTC	AAGCAGTTCC	TCGTGGCCCA	GAAGAACGAG	60
GGCCGGCAGA	TTTTCCCTCG	CGGGCCTGAG	TATTTTCGCG	CGCTCGACCT	GACGCCGCTC	120
GACAAGGTGC	GCGTGGTTCAT	TCTCGGCCAG	GATCCCTATC	ACGGTGACGG	CCAGCGGCAT	180
GGGCTCTGCT	TCAGCGTTTCG	CCCCGGTGTC	CGGACGCCGC	CGTCGCTGGT	CAACATCTAC	240
AAGGAACTGA	ATACCGATCT	CGGTATTCCG	CCGGCGCGTC	ACGGTTTTCT	CGAAAGCTGG	300
GCAAGGCAGG	GCGTGCTGCT	TTTGAACAGC	GTGCTGACGG	TAGAGCGCGG	GAACGTGCGT	360
CACACCAGGG	TCACGGTTGG	GAAAAGTTCA	CGGATGCGAT	CATCCGTGCG	GTCAACGAGG	420
CCGAGCATCC	CGTCGTCTTC	ATGCTTTGGG	GCTCCTATGC	GCAGAAGAAG	GCGGCCTTCG	480
TCGACCGCTC	GCGCCATCTT	GTCTTGAGGG	CACCACATCC	CTCGCCGCTC	TCAGCCCATT	540
CCGGCTTTCT	CGGCTGCCGG	CATTTTTC	AGGCCAATGC	CTTCCTCGAA	AGCAAAGGCT	600
TCGATCCGAT	CGACTGGCGG	CTGCCGGA	ATCCGGCTGC	GGACATCAAC	TGAAGGCTTG	660
GCGCGAATGA	CGGCTTTGTC	GTGCCCCTGA	GGTCTTGCTT	TGGCGGCGGC	GATCCGCCTA	720
AGACGCCCCA	ACGAAATGGC	GGAGGCGGGC	ATGCGCAAAA	TTCTGATCAT	CGGCATCGGT	780
TCGGGCAATC	CCGAACACAT	GACCGTGACG	GCGATCAACG	CGTGAACTG	CGCCGACGTG	840
CTCTTTATCC	CGACCAAGGG	AGCGAAGAAG	ACCGAGCTTG	CCGAAGTGCG	CCGCGACATC	900
TGCGCCCGCT	ACGTCAACGC	CAAGGACAGC	CGCACCGTCG	AGTTCGCGGT	GCCCGTGCGG	960
CGCACCGAAG	GCGTCAGCTA	TGACGGCAGC	GTGATGACT	GGCACGCCCA	GATCGCTGGG	1020
ATTTACGAAG	CGCTTCTATC	GAAGGAGTTG	GGCGAAGAGG	GAAGTGGCGC	GTTTCTCGTC	1080
TGGGGCGACC	CGATGCTCTA	TGACAGCACC	ATTGCGATCG	TCGAGCGGGT	CAAGGCACGC	1140
GGTGAGGTCG	CCTTCGCCTA	CGACGTCATT	CCCGGGATCA	CCAGTCTGCA	GGCGCTTTGC	1200
GCCAGCCACC	GCATTCCGCT	GAACCTCGTC	GGCAAGCCGG	TGGAGATCAC	CACGGGGCGT	1260
CGGCTGCACG	AAAGCTTTCC	CGAGAAGAGC	CAGACCTCGG	TCGTATGCT	CGATGGCGAA	1320
CAGGCGTTTC	AGCGGGTCGA	GGACCCGGAG	GCGGAGATCT	ATTGGGGCGC	CTATCTCGGC	1380
ACGCGGGATG	AGATCGTCAT	TTCCGGCCGC	GTGGCTGAGG	TGAAGGACCG	GATCCTTGAA	1440
ACGCGGGCGG	CGGCGCGCGC	GAAGATGGGA	TGGATCATGG	ACATCTATCT	CCTGCGCAAG	1500
GGCGCCGACT	TCGACGAGTG	ACGGGGAGGG	CCGATCTGCG	TCGTGTTTGA	TCTCACTCAA	1560
GGTTTGCGGC	TGTGTTATAG	CGCTTTAAGA	GCTTCTTCA	GGGAGGAGAA	CCTCAAGTGA	1620
TGACGGAATT	GATGACCAGC	TGCGCCCTTC	CATTGACCGG	AGATGCCGGC	ACCGTCGCTT	1680
CGATGCGCCG	CGGCGCCTGC	CCGTCTTTGG	CAGAGCCGAT	GCAGACCGGC	GACGGCCTGC	1740
TCGTGAGGGT	GAGGCCAACG	GATGACAGCC	TGACGCTGCC	GAAGGTCATT	GCCCTTGCCA	1800
CGGCTGCCGA	GCGCTTCGGC	AATGGCATCA	TCGAGATTAC	CGCGCGCGGA	AACCTGCAGC	1860
TTGCGGGCCT	GAGCGCGGCT	TCGGTGCCAA	GGCTGGCGCA	GGCGATCGGC	GATGCGGAGA	1920
TCGCCATTGC	CGAGGGGCTC	GCGATCGAGG	TGCCGCCCTT	GGCCGGCATC	GACCCGGACG	1980
AGATCGCCGA	TCCGCGGCCG	ATTGCCACTG	AGCTTCGTGA	AGCGTTGGAT	GTGCGCCAGG	2040

TGCCGTTGAA	GCTTGCACCC	AAATTATCCG	TCGTCATCGA	TAGCGGTGGC	CGGTTTGGTC	2100
TCGGCGCTGT	CGTCGCCGAC	ATTGCGCTTC	AGGCGGTTTC	GA CTGTGCGG	GGGGTGGCCT	2160
GGGTGCTGTC	GCTTGGCGGC	ACGTCAACGA	AGGCATCGAG	CGTCGGGACG	TTGGCCGGCA	2220
ACGCGGTCTG	GCCGGCCCTG	ATCACCATTTC	TCGAGAAACT	GGCGAGCCTG	GGCACGACGA	2280
TGCGCGGGCG	CGATCTGGAC	CCGTGCGAAA	TCCGCGCGCT	CTGTGCTGT	GAGACATCGT	2340
CCGAACGCCC	GGCCGCTCCG	CGTTGCGCCG	CAATACCCGG	CATTCATGCG	CTGGGTAACG	2400
CCGACACCGT	TCTCGGCCTC	GGTCTGGCCT	TTGCTCAGGT	GGAGGCCGCC	GCGCTGGCAT	2460
CCTACCTGCA	TCAGGTCCAG	GCGCTTGGCG	CCAATGCGAT	CCGGCTTGCG	CCCGGGCACG	2520
CCTTCTTCGT	CCTCGGCCTT	TGCCCCGAGA	CCGCGGCTGT	GGCGCAGAGC	CTGGCAGCGT	2580
CACACGGTTT	TCGCATTGCC	GAGCAGGATC	CGCGCAATGC	GATCGCCACC	TGCGCCGGCA	2640
GCAAGGGTTG	CGCTCGGCG	TGGATGGAAA	CCAAGGGCAT	GGCCGAGCGC	CTCGTCGAGA	2700
CGGCGCCGGA	ATTGCTCGAC	GGGTGCTCA	CCGTGCATCT	CTCCGGCTGC	GCCAAGGGCT	2760
GCGCCCGGCC	GAAGCCGTCC	GAAGTACGC	TTGTGCGTGC	GCCATCAGGA	TACGGGCTTG	2820
TCGTAAATGG	GGCTGCCAAT	GGCTTGCCAA	GCGCTACAC	CGATGAGAAT	GGAATGGGAT	2880
CCGCCCTTGC	CCGGCTCGGC	CGGCTGGTGC	GGCAAAACAA	AGACGCTGGC	GAATCGGCGC	2940
AGTCCTGTCT	TACACGGCTC	GGAGCTGCGC	GCGTCTCGGC	AGCGTTTCGAA	CAGGGATAGA	3000
CATGCCTGAG	TATGATTACA	TTGCGGATGG	CAACGCCATC	TACGAGCGTT	CCTTCGCCAT	3060
CATCCGCGCC	GAGGCCGATC	TGTCGCGCTT	CTCCGAAGAG	GAAGCGGATC	TGGCTGTGCG	3120
CATGGTGAC	GCCTGCGGTT	CCGTGAGGGC	GACCAGGCAG	TTGCTGTTTT	CTCCCGATTT	3180
CGTAAGCTCG	GCCCCGTCCG	CGCTGAAAGC	CGGTGCGCGG	ATCCTCTGCG	ATGCCGAGAT	3240
GGTTGCGCAC	GGTGTACCC	GCGCCCGTCT	GCCGGCCGGC	AACGAGGTGA	TCTGCACGCT	3300
GCGCGATCCT	CGCACGCCCG	CACTTGCGGC	CGAGATCGGC	AACACCCGCT	CCGCCGCGAGC	3360
CCTGAAGCTC	TGGAGCGAGC	GGCTGGCCGG	TTGCGTGGTC	GCGATCGGCA	ACGCGCCGAC	3420
GGCGTTGTTT	TTCTCTTTGG	AAATGCTGCG	CGACGGCGCG	CCGAAGCCGG	CGGCAATCCT	3480
CGGCATGCCC	GTCGGTTTTG	TCGGTGCGGC	GGAATCGAAG	GATGCGCTGG	CCGAGAACTC	3540
CTATGGCGTT	CCCTTCGCCA	TCGTGCGCGG	CCGCCTCGGC	GGGAGTGCCA	TGACGGCGGC	3600
AGCGCTTAAC	TCGCTCGCGA	GGCCGGGCCT	GTGAGCGGCG	TCGGCGTGGG	GCGCCTGATC	3660
GGTGTGGA	CCGGCCCCGG	TGATCCGGAA	CTTTTGACGG	TCAAGGCGGT	GAAGGCGCTC	3720
GGGCAAGCCG	ATGTGCTTGC	CTATTTGCGC	AAGGCCGGGC	GAAGCGGTAA	CGGCCGCGCG	3780
GTGGTCGAGG	GTCTGCTGAA	GCCCCGATCTT	GTCGAGCTGC	CGCTATACTA	TCCGGTGACG	3840
ACCGAAATCG	ACAAGGACGA	TGGCGCCTAC	AAGACCCAGA	TCACCGACTT	CTACAATGCG	3900
TCGGCCGAAG	CGTACGCGG	GCATCTTGCC	GCCGGGCGCA	CGGTGCGCGT	GCTCAGTGAA	3960
GGCGACCCGC	TGTTCTATGG	TTCTTACATG	CATCTGCATG	TGCGGCTCGC	CAATCGTTTT	4020
CCGGTCGAGG	TGATCCCCGG	CATTACCGCC	ATGTCCGGCT	GTTGGTCGCT	TGCCGGCCTG	4080
CCGCTGGTGC	AGGGCGACGA	CGTGCTCTCG	GTGCTTCCGG	GCACCATGGC	CGAGGCCGAG	4140
CTCGGCCGCA	GGCTTGCGGA	TACCGAAGCC	GCCGTGATCA	TGAAGGTCGG	GCGCAATTTG	4200
CCGAAGATCC	GTCGGGCGCT	CGCTGCCTCC	GGCCGTCTCG	ACCAGGCCGT	CTATGTCGAA	4260
CGGACGACGA	TGAAGAACGC	GGCGATGACG	GCTCTTGCGG	AAAAGGCCGA	CGACGAGGCG	4320
CCCTATTTCT	CGTGGTGCT	CGTTCCCGGC	TGGAAGGACC	GACCATGACC	GGTACGCTCT	4380
ATGTGCTCGG	TACCGGACCG	GGCAGCGCCA	AGCAGATGAC	GCCGGAAACG	GCGGAAGCCG	4440
TTGCGGCCGC	TCAGGAGTTT	TACGGCTACT	TTCCCTATCT	CGACCGGCTG	AACCTCAGAC	4500
CGGATCAGAT	CCGTGTCGCC	TCGGACAACC	GCGAGGAGCT	CGATCGGGCA	CAGGTGCGGC	4560
TGACGCGGGC	TGCGGCAGGC	GTGAAGGTCT	GCATGGTCTC	CGGTGGCGAT	CCCGGTGTCT	4620
TTGCCATGGC	GGCCGCCGTC	TGCGAGGCGA	TCGACAAGGG	ACCGGCCGAA	TGGAAGTCGG	4680
TTGAAGTGGT	GATCACGCCC	GGCGTGACCG	CGATGCTCGC	CGTTGCCGCC	CGCATCGGCG	4740
CGCCGCTCGG	TCATGATTTT	TGTGCGATCT	CGCTTTCCGA	CAATCTGAAG	CCCTGGGAAG	4800
TCATCACCCG	GCGTCTCAGG	CTGGCGGCGG	AAGCGGGCTT	CGTCATTGCC	CTCTACAATC	4860
CGATCAGCAA	GGCGCGGCCC	TGGCAGCTCG	GTGAGGCCTT	CGAGCTTCTG	GCGAGCGTTC	4920
TGCCGGCAAG	CGTTCCGGTC	ATCTTCGGCC	GTGCGGCCGG	GCGGCCGGAC	GAACGGATCG	4980
CGGTGATGCC	GCTCGGCGAG	GCCGATGCCA	ACCGCGCCGA	CATGGCGACC	TGCGTCATCA	5040
TCGGCTCGCC	GGAGACGCGC	ATCGTCGAGC	GCGACGGCCA	ACCCGATCTC	GTCTACACAC	5100
CGCGCTTCTA	TGCAGGGGCG	AGCCAGTGAG	CGATGCGGTT	GAGTGCCTCG	TCGCAACTGC	5160
CGACCGTCGG	CACGTCCGCG	GGCTTGCGCC	GCTCGACCAT	GATCACCTCG	ATGCCGAGCC	5220
GGCGCGCTGC	GGCAATCTTG	CCGTAGGTGG	CGCTGCCACC	GCTGTTCTTG	GCGACGATCA	5280
CATCGATCTG	CCGACTCTGT	AGCAACGCGG	CTTCGTGCGG	TTCCGCAAAG	GGACCGGTCTG	5340
CCAGGATCGC	CTCTGGTTCG	GGCAGATTAA	GCGGCGGCGT	CACCGGATCG	ACGCTGCGGA	5400
TGACGTAGCT	GTGCTGCGGC	GCGACCTCGA	AGTGGAAGAG	TTCTGTCTGA	CCTATCGCCA	5460
GGAAGACGCG	GCGTCGCCGA	TCACCGAGCG	CGCTGACGGC	CTCGACAACG	CTATCGACAG	5520
CAGTCCAGCG	GTCGCCAGGC	AGGGGCACCC	ATTCCGGTCG	GCGGAGGGCG	ATAAGCGCAA	5580
CGCCGGTTCT	TTGCGCTGCG	TCCGCGGCGT	TGTGCGAAAT	GCGTGCGGCA	AAGGGGTGCG	5640
TCGCATCGAC	CAGCAGCGCG	ATGTTTTCTG	CATGCACGAA	ATGCGCCAGC	CCATCCGCGC	5700
CGCAAAGACC	GCGGATGCGC	GTCTTGACCG	GTCGCGGCGG	CGGGTCCGCG	GTGCGGCCGG	5760
CCAGCGAGAT	GGCGGTGTCTG	TAGCGGACAT	CTTCGGCCAA	GCGGCGCGCG	AGTTGCGGTG	5820

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CCTCGGTGGT	GCCACCCAGA	ATCAGAATAC	GAGGTTTTTC	CATGGCTGAC	GTGTCGAACA	5880
GCGAACC CGC	CATAGTCTCC	CCCTGGCTGA	CCGTCACTCG	TATCGGTGAG	GATGGTGTAG	5940
CGGGTCTCGG	CGACGAGGCC	AAGCGGCTGA	TCGCCGAAGC	GCCGGTCGTC	TACGGCGGCC	6000
ATCGTCATCT	GGAGCTCGCC	GCCTCCCTCA	TCACCGGCGA	AGCGCACAAAT	TGGCTAAGCC	6060
CCCTCGAACG	CTCGGTCTGC	GAGATCGTCG	CGCGTCGCGG	CAGCCCGGTG	GTGGTGCTTG	6120
CCTCGGGCGA	CCCGTTCTTC	TTCCGGCGTCG	GCGTGACGCT	GGCGCGCCGC	ATCGCCTCGG	6180
CCGAAATACG	CACGCTTCCG	GCGCCGTCGT	CGATCAGTCT	TGCCGCTCG	CGCCTCGGCT	6240
GGGCGCTGCA	GGATGCGACG	CTCGTCTCCG	TACATGGGCG	GCCGCTGGAT	CTGGTGCGAC	6300
CGCATTTGCA	TCCGGGGGCG	CGTGTGCTTA	CGCTCACGTC	GGACGGTGCG	GGTCCGCGAG	6360
ACCTTGCCGA	GCTTCTGGTT	TCAAGCGGCT	TCGGTCAGTC	GCGACTGACC	GTGCTCGAAG	6420
CGCTGGGCGG	CGCCGGCGAA	CGGGTGACGA	CGCAGATCGC	CGCGCGCTTC	ATGCTCGGCC	6480
TCGTGCATCC	TTTGAACGTC	TGCGCCATTG	AGGTGGCGGC	CGACGAGGGC	GCGCGCATCC	6540
TGCCGCTTGC	CGCCGGCCGC	GACGATGCGC	TGTTCTGAACA	TGACGGGCAG	ATCACCAAGC	6600
GCGAGGTGCG	GGCGCTGACG	CTGTGCGCAC	TCGCACCGCG	CAAGGGCGAA	CTGCTATGGG	6660
ACATCGGCGG	CGGCTCCGGC	TCGATCGGCA	TCGAATGGAT	GCTCGCCGAT	CCGACCATGC	6720
AGGCGATCAC	CATCGAGGTT	GAGCCGGAGC	GGGCAGCGCG	CATCGGCCGC	AACGCGACGA	6780
TGTTGCGCGT	GCCCCGGGCTG	ACGGTTGTCTG	AAGGCGAGGC	GCCGGCGGCG	CTTGCCGGCC	6840
TGCCACAACC	GGACGCGATC	TTTCATCGGCG	GCGGCGGCAG	CGAAGACGGC	GTCATGGAAG	6900
CAGCGATCGA	GGCGCTCAAG	TCAGGCGGAC	GGCTGGTTGC	CAACGCGGTG	ACGACGGACA	6960
TGGAAGCGGT	GCTGCTCGAT	CATCACGCGC	GGCTCGGCGG	TTGCTGATC	CGCATCGATA	7020
TCGCGCGTGC	AGGACCCATC	GGCGGCATGA	CCGGCTGGAA	GCCGGCCATG	CCGGTCACCC	7080
AATGGTCTGT	GACGAAGGGC	TAAAGCAGTT	CCAGCGAAAG	TGTGACGCGG	TTTTGCGTCC	7140
GGAACTGCGC	AAGAAAAAGA	AAGAGTAACC	TATGACGGTA	CATTTTCATCG	GCGCCGGCCC	7200
GGGAGCCGCA	GACCTGATCA	CGGTGCGTGG	TCGCGACCTG	ATCGGGCGCT	GCCCCGTCTG	7260
CCTTTACGCC	GGCTCGATCG	TCTCGCCGGA	GCTGCTGCGA	TATTGCCCGC	CGGGCGCCCG	7320
CATTGTGCGT	ACGGCGCCGA	TGTCCCTCGA	CGAGATCGAG	GCGGAGTATG	TGAAGGCCGA	7380
AGCCGAAGGG	CTCGACGTGG	CGCGGCTTCA	TTGCGGCGAC	CTTTCGGTCT	GGAGTGCTGT	7440
GGCCGAACAG	ATCCGCCGGC	TCGAGAAGCA	TGGCATCGCC	TATACGATGA	CGCCGGGCGT	7500
TCCTTCCTTT	GCGGCGGCGG	CTTCAGCGCT	CGGTGCGGAA	TTGACCATTG	CGGCCGTGGC	7560
CCAGAGCCTG	GTGCTGACCC	GCGTTTCGGG	CCGCGCCTCG	CCGATGCCGA	ACTCAGAAAC	7620
GCTTTCGGCT	TTCCGGCGCTA	CGGGATCGAC	GCTGGCAATC	CACCTTGCGA	TCCATGCGCT	7680
TCAGCAGGTG	GTCGAGGAAC	TGACGCCGCT	CTACGGTGCC	GACTGCCCCG	TCGCCATCGT	7740
CGTCAAGGCC	TCCTGGCCGG	ACGAACGCGT	GGTGCGCGGC	ACGCTCGGTG	ACATCGCCGC	7800
CAAGGTGGCG	GAAGAGCCGA	TCGAGCGCAC	GGCGCTGATC	TTGCTCGGTC	CGGGGCTCGA	7860
AGCCTCCGAT	TTCCGTGAAA	GCTCGCTCTA	CGATCCCGCC	TATCAGCGGC	GCTTCAGAGG	7920
GCGCGGCGAA	TAGGCCGCGC	TCCCTCGGGG	GTCGGCCTAA	GTTTCCCGCT	GAGAGGGTTT	7980
TGAAACCTAT	TCTGCCGGTT	CTTCGCGCGG	CGGCCGCTGC	TTGAGCGGGA	CGCCGCGCTT	8040
TTCTTCGACG	CGGTGCGGCT	AGAGCGCTGC	CTGTCCAAGC	AGCATCAGCG	TCACCGGCGT	8100
GGTGGCGACG	ACGAAGACGA	TGATCAGGAT	TTCTGTGGAAT	ACCCAGCGGC	TCTGCAGCAC	8160
GGCAAAGCAG	ATGATAGAGG	CGGCGCAGAT	CATCAGTACG	CCGCCGCTGG	TCGCCAGCGT	8220
CGGTGCGTGC	AGGCGCTCGT	AGAAGCTGGT	GAACCGGAGC	AAGCCGACGG	AGCCGATCAG	8280
CGCCACTGCG	GCGCCGAGGA	CGGTGAGCCC	GCAGACGAGA	ACGGCTGCCC	AGACGGGAAG	8340
GTCGGTGAGG	TGGCTCATTC	GATGATCTCC	CCGCGCATCA	GGAACCTTGCC	GAAGGCGATC	8400
GACGAGACGA	AGCCGATCAA	AGCCACGATC	AGGGCGGACT	CGAAATAGAG	CGAGTTGGCC	8460
GTGCGGATGC	CGAAGGTCAA	GAGCATCAGC	ATGGCGTTGA	TATAGAGCGT	GTGAGGCCG	8520
AGGATACGGT	CCTGGGCGCG	CGGTCCCCTC	ACCATGCGAT	AGAAGGCAAA	AGCCATCGCC	8580
AGGCCGAGCA	TGATCTGGGC	AATCAGGATC	GACCAGATGA	TTGAAAGTTC	CATCATCCGA	8640
ATATCTCCTT	CAGGGCGGTC	TCATAGCGCT	TGACCGTATC	GAGCCAGATG	TCCTCGTTCT	8700
CCATGTCGAG	CACGTGGAAG	AGCAGGGACT	TGCGGCCGCG	ATCCGGGGAA	TTC	8753

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 843 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cdna
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:

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- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

- (ix) FEATURE:
- (A) NAME/KEY: *cobA*
 - (B) LOCATION: 1141-1980 bp of SEQ ID NO: 1
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATGATCGACG	ACCTCTTTGC	CGGATTGCCG	GCGCTCGAAA	AAGGTTTCGGT	CTGGCTGGTC	60
GGCGCCGGCC	CCGGCGATCC	CGGCCTGTTG	ACGCTGCATG	CGGCCAATGC	GCTGCGCCAG	120
GCGGATGTGA	TCGTGCATGA	TGCGCTGGTC	AACGAGGATT	GCCTGAAGCT	CGCGCGGCCG	180
GGCGCCGTGC	TGGAGTTTGC	GGGCAAGCGT	GGCGGCAAGC	CGTCGCCGAA	GCAGCGCGAC	240
ATCTCGCTTC	GCCTCGTCGA	ACTCGCGCGC	GCCGGCAACC	GGGTGCTGCG	CCTCAAAGGC	300
GGCGATCCCT	TCGTCTTCGG	TCGCGGTGGC	GAGGAGGCGC	TGACGCTGGT	CGAACACCAG	360
GTGCCGTTCC	GAATCGTGCC	CGGCATCACC	GCCGGTATCG	GCGGGCTTGC	CTATGCCGGC	420
ATTCCCGTGA	CCCATCGCGA	GGTCAACCAC	GCGGTCACTT	TCCTGACTGG	CCATGATTCC	480
TCCGGCCTGG	TGCCGGATCG	CATCAACTGG	CAGGGCATCG	CCAGCGGCTC	GCCTGTCATC	540
GTCATGTACA	TGGCGATGAA	ACATATCGGC	GCGATCACCG	CCAACCTCAT	TGCCGGCGGC	600
CGCTCGCCGG	ACGAACCGGT	CGCCTTCGTC	TGCAACGCCG	CGACGCCGCA	GCAGGCGGTG	660
CTGGAAACGA	CGCTTGCGCG	TGCAGAGGCC	GATGTTGCGG	CGGCAGGGCT	GGAGCCGCCG	720
GCGATCGTCG	TCGTGCGCGA	GGTGGTGCGG	CTGCGCGCAG	CGCTCGACTG	GATCGGCGCG	780
CTGGACGGGC	GCAAGCTTGC	CGCCGACCCG	TTCGCCAATC	GCATTCTCAG	GAACCCGGCA	840
TGA						843

- (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 280 amino acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
- (A) ORGANISM: *Pseudomonas denitrificans*
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:

- (ix) FEATURE:
- (A) NAME/KEY: COBA
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION: Translation product of SEQ ID NO:3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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Met Ile Asp Asp Leu Phe Ala Gly Leu Pro Ala Leu Glu Lys Gly Ser
1      5      10      15
Val Trp Leu Val Gly Ala Gly Pro Gly Asp Pro Gly Leu Leu Thr Leu
20      25      30
His Ala Ala Asn Ala Leu Arg Gln Ala Asp Val Ile Val His Asp Ala
35      40      45
Leu Val Asn Glu Asp Cys Leu Lys Leu Ala Arg Pro Gly Ala Val Leu
50      55      60
Glu Phe Ala Gly Lys Arg Gly Gly Lys Pro Ser Pro Lys Gln Arg Asp
65      70      75      80
Ile Ser Leu Arg Leu Val Glu Leu Ala Arg Ala Gly Asn Arg Val Leu
85      90      95
Arg Leu Lys Gly Gly Asp Pro Phe Val Phe Gly Arg Gly Gly Glu Glu
100     105     110
Ala Leu Thr Leu Val Glu His Gln Val Pro Phe Arg Ile Val Pro Gly
115     120     125
Ile Thr Ala Gly Ile Gly Gly Leu Ala Tyr Ala Gly Ile Pro Val Thr
130     135     140
His Arg Glu Val Asn His Ala Val Thr Phe Leu Thr Gly His Asp Ser
145     150     155     160
Ser Gly Leu Val Pro Asp Arg Ile Asn Trp Gln Gly Ile Ala Ser Gly
165     170     175
Ser Pro Val Ile Val Met Tyr Met Ala Met Lys His Ile Gly Ala Ile
180     185     190
Thr Ala Asn Leu Ile Ala Gly Gly Arg Ser Pro Asp Glu Pro Val Ala
195     200     205
Phe Val Cys Asn Ala Ala Thr Pro Gln Gln Ala Val Leu Glu Thr Thr
210     215     220
Leu Ala Arg Ala Glu Ala Asp Val Ala Ala Ala Gly Leu Glu Pro Pro
225     230     235     240
Ala Ile Val Val Val Gly Glu Val Val Arg Leu Arg Ala Ala Leu Asp
245     250     255
Trp Ile Gly Ala Leu Asp Gly Arg Lys Leu Ala Ala Asp Pro Phe Ala
260     265     270
Asn Arg Ile Leu Arg Asn Pro Ala
275     280

```

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1305 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 (A) ORGANISM: *Pseudomonas denitrificans*
 (B) STRAIN:
 (C) INDIVIDUAL ISOLATE:
 (D) DEVELOPMENTAL STAGE:
 (E) HAPLOTYPE:
 (F) TISSUE TYPE:
 (G) CELL TYPE:
 (H) CELL LINE:

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(I) ORGANELLE:

(ix)

FEATURE:

- (A) NAME/KEY: cobb
- (B) LOCATION: 1980-3283 bp of SEQ ID NO: 1
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGAGCGGAT	TGCTGATTGC	CGCACCCGCG	TCCGGCTCCG	GCAAGACGAC	GGTGACGCTC	60
GGGCTGATGC	GCGCCCTGAA	GAGGCGCGGC	GTGGCGATCG	CGCCCCGGCA	GGCGGGGCCG	120
GACTATATCG	ATCCCCGTTT	CCACGCGGCA	GCGACCGGCG	AGCCCTGCTT	CAACTACGAC	180
CCCTGGGCGA	TGCGCCCGGA	ACTGCTGCTT	GCCAATGCGT	CGCATGTGGC	CTCCGGCGGG	240
CGCACATTGA	TCGTCGAGGC	GATGATGGGA	CTGCATGACG	GTGCTGCCGA	CGGCTCGGGA	300
ACGCCAGCGG	ACCTCGCCGC	GACGCTGAAC	CTTGCGGTCA	TTCTGGTGGT	CGATTGCGCC	360
CGCATGTCCC	AGTCGGTTGC	CGCCCTCGTG	CGCGGCTATG	CGGATCATCG	CGACGATATC	420
CGGGTGGTTG	GCGTCATCCT	CAACAAGGTC	GGCAGCGATC	GGCATGAAAT	GATGCTGCGC	480
GATGCGCTCG	GCAAGGTGCG	CATGCCTGTC	TTCGGCGTGC	TCCGGCAGGA	CAGCGCATTG	540
CAACTGCCGG	AGCGCCATCT	CGGGCTCGTG	CAGGCGGGCG	AACACTCAGC	GCTTGAGGGC	600
TTCATCGAGG	CGGCGGCCGC	GCGGGTCGAG	GCTGCCTGCG	ATCTCGACGC	CATCCGCCTG	660
ATCGCGACGA	TTTTCCCGCA	GGTGCCCGCG	GCGGCCGATG	CCGAGCGTTT	GCGGCCGCTC	720
GGTCAGCGCA	TCGCGGTGCG	GCGCGATATC	GCCTTTGCCT	TCTGCTACGA	GCACCTGCTT	780
TACGGCTGGC	GGCAAGGCGG	CGCGGAGATT	TCCTTCTTCT	CGCCGCTCGC	CGACGAGGGG	840
CCGGATGCGG	CAGCCGATCG	CGTCTATCTT	CCGGGGGGTT	ATCCGGAGCT	GCATGCGGGG	900
CAGCTGAGCG	CCGCCGCCCG	ATTCCGTTCC	GGCATGCATT	CCGCGGCGGA	ACGCGGCGCC	960
CGCATCTTCG	GCGAGTGCGG	CGGCTATATG	GTGCTCGGCG	AAGGGCTTGT	CGCTGCCGAT	1020
GGCACACGCT	ACGACATGCT	CGGCCTGCTG	CCGCTCGTAA	CCAGTTTTGC	CGAGCGCAGG	1080
CGGCACCTCG	GCTATCGCCG	CGTCGTGCCT	GTCGACAACG	CCTTCTTCGA	TGGACCCATG	1140
ACGGCGCACG	AATTCCACTA	TGCGACCATC	GTCGCCGAAG	GGGCGGCCGA	TGGGCTGTTT	1200
GCGGTCAGCG	ACGCCGCCCG	CGAGGATCTC	GGCCAGGCGG	GCCTCCGGCG	CGGCCCTGTC	1260
GCCGGTTCCT	TCATGCATCT	GATCGACGTC	GCAGGTGCTG	CATGA		1305

(2) INFORMATION FOR SEQ ID NO: 6:

(i)

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii)

MOLECULE TYPE: protein

(iii)

HYPOTHETICAL: No

(iv)

ORIGINAL SOURCE:

- (A) ORGANISM: Pseudomonas denitrificans
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix)

FEATURE:

- (A) NAME/KEY: COBB
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:5

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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Met	Ser	Gly	Leu	Leu	Ile	Ala	Ala	Pro	Ala	Ser	Gly	Ser	Gly	Lys	Thr
1				5					10					15	
Thr	Val	Thr	Leu	Gly	Leu	Met	Arg	Ala	Leu	Lys	Arg	Arg	Gly	Val	Ala
			20					25					30		
Ile	Ala	Pro	Gly	Lys	Ala	Gly	Pro	Asp	Tyr	Ile	Asp	Pro	Ala	Phe	His
		35					40				45				
Ala	Ala	Ala	Thr	Gly	Glu	Pro	Cys	Phe	Asn	Tyr	Asp	Pro	Trp	Ala	Met
		50				55					60				
Arg	Pro	Glu	Leu	Leu	Leu	Ala	Asn	Ala	Ser	His	Val	Ala	Ser	Gly	Gly
65				70						75					80
Arg	Thr	Leu	Ile	Val	Glu	Ala	Met	Met	Gly	Leu	His	Asp	Gly	Ala	Ala
			85						90					95	
Asp	Gly	Ser	Gly	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Thr	Leu	Asn	Leu	Ala
			100					105					110		
Val	Ile	Leu	Val	Val	Asp	Cys	Ala	Arg	Met	Ser	Gln	Ser	Val	Ala	Ala
		115					120					125			
Leu	Val	Arg	Gly	Tyr	Ala	Asp	His	Arg	Asp	Asp	Ile	Arg	Val	Val	Gly
	130					135					140				
Val	Ile	Leu	Asn	Lys	Val	Gly	Ser	Asp	Arg	His	Glu	Met	Met	Leu	Arg
145				150						155					160
Asp	Ala	Leu	Gly	Lys	Val	Arg	Met	Pro	Val	Phe	Gly	Val	Leu	Arg	Gln
			165					170					175		
Asp	Ser	Ala	Leu	Gln	Leu	Pro	Glu	Arg	His	Leu	Gly	Leu	Val	Gln	Ala
		180						185					190		
Gly	Glu	His	Ser	Ala	Leu	Glu	Gly	Phe	Ile	Glu	Ala	Ala	Ala	Ala	Arg
		195					200					205			
Val	Glu	Ala	Ala	Cys	Asp	Leu	Asp	Ala	Ile	Arg	Leu	Ile	Ala	Thr	Ile
	210					215					220				
Phe	Pro	Gln	Val	Pro	Ala	Ala	Ala	Asp	Ala	Glu	Arg	Leu	Arg	Pro	Leu
225				230					235						240
Gly	Gln	Arg	Ile	Ala	Val	Ala	Arg	Asp	Ile	Ala	Phe	Ala	Phe	Cys	Tyr
			245					250						255	
Glu	His	Leu	Leu	Tyr	Gly	Trp	Arg	Gln	Gly	Gly	Ala	Glu	Ile	Ser	Phe
		260					265						270		
Phe	Ser	Pro	Leu	Ala	Asp	Glu	Gly	Pro	Asp	Ala	Ala	Ala	Asp	Ala	Val
		275					280					285			
Tyr	Leu	Pro	Gly	Gly	Tyr	Pro	Glu	Leu	His	Ala	Gly	Gln	Leu	Ser	Ala
	290					295					300				
Ala	Ala	Arg	Phe	Arg	Ser	Gly	Met	His	Ser	Ala	Ala	Glu	Arg	Gly	Ala
305				310					315						320
Arg	Ile	Phe	Gly	Glu	Cys	Gly	Gly	Tyr	Met	Val	Leu	Gly	Glu	Gly	Leu
			325					330						335	
Val	Ala	Ala	Asp	Gly	Thr	Arg	Tyr	Asp	Met	Leu	Gly	Leu	Leu	Pro	Leu
		340						345					350		
Val	Thr	Ser	Phe	Ala	Glu	Arg	Arg	Arg	His	Leu	Gly	Tyr	Arg	Arg	Val
		355					360					365			
Val	Pro	Val	Asp	Asn	Ala	Phe	Phe	Asp	Gly	Pro	Met	Thr	Ala	His	Glu
	370					375					380				
Phe	His	Tyr	Ala	Thr	Ile	Val	Ala	Glu	Gly	Ala	Ala	Asp	Arg	Leu	Phe
385				390					395						400
Ala	Val	Ser	Asp	Ala	Ala	Gly	Glu	Asp	Leu	Gly	Gln	Ala	Gly	Leu	Arg
			405					410						415	
Arg	Gly	Pro	Val	Ala	Gly	Ser	Phe	Met	His	Leu	Ile	Asp	Val	Ala	Gly
			420					425					430		
Ala	Ala														

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1002 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Unknown

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- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas denitrificans*
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:
- (ix) FEATURE:
(A) NAME/KEY: cobC
(B) LOCATION: 3281-4279 bp of SEQ ID NO: 1
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATGAGCGCAC	CGATCGTTCA	TGGTGGCGGC	ATCACCGAGG	CCGCAGCGCG	CTATGGCGGC	60
CGGCCTGAAG	ACTGGCTCGA	TCTGTCGACC	GGCATCAATC	CATGCCCCGT	CGCCTTGCCC	120
GCGGTCCCTG	AGCGCGCCTG	GCACCGGCTG	CCGGATCGGC	AGACGGTAGA	TGATGCGCGG	180
AGCGCCGCCG	CCGACTACTA	CCGCACCAAC	GGCGTGCTGC	CTTTGCCGGT	GCCGGGCACC	240
CAGTCGGTGA	TCCAGCTCCT	GCCACGTCTT	GCTCCGGCCA	ACAGGCACGT	CGCGATTTTC	300
GGGCCGACCT	ATGGCGAGTA	TGCCCCGCGT	CTTGAAGCGG	CCGGCTTTGC	TGTCGATCGC	360
GTCGCGGATG	CCGACGCGCT	CACGGCCGAA	CATGGGCTTG	TCATCGTCGT	CAACCCCAAC	420
AACCCGACCG	GCCGCGCCTT	GGCGCCGGCG	GAGCTTCTGG	CGATCGCCGC	AAGGCAGAAG	480
GCGAGCGGCG	GACTGCTGCT	GGTCGATGAG	GCCTTCGGCG	ATCTTGAGCC	GCAACTGAGT	540
GTCGCTGGTC	ACGCGTCAGG	GCAAGGCAAC	CTCATCGTCT	TCCGCTCCTT	CGGCAAGTTC	600
TTCGGCCTTG	CGGGCCTGCG	CCTCGGCTTC	GTCGTTGCGA	CCGAGCCAGT	GCTTGCATCC	660
TTTGCCGATT	GGCTCGGTCC	CTGGGCTGTC	TCCGGCCCCG	CGTTGACGAT	CTCGAAAGCG	720
CTGATGCAGG	GCGATACGAA	GGCGATCGCG	GCGGGCATCC	TCGAGCGTCG	CGCCGGCCTC	780
GATGCGGCTC	TCGATGGGGC	AGGGCTCAAC	CGTATCGGCG	GCACGGGGCT	ATTCGTGCTG	840
GTCGAGCATC	CCAGGGCAGC	TCTGCTGCAG	GAGCGGCTCT	GCGAGGCCCA	TATTCTCACG	900
CGCAAGTTTC	ACTATGCCCC	GACCTGGCTC	AGGGTCGGTC	TTGCGCCTGA	CGCGGCTGGT	960
GACCGACGGC	TGGCGGACGC	GCTTGCCCCG	ATGGAGCTCT	GA		1002

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 amino acids
(B) TYPE: Amino Acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas denitrificans*
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:

10724598

(I) ORGANELLE:

(ix)

FEATURE:

- (A) NAME/KEY: COBC
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:7

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met	Ser	Ala	Pro	Ile	Val	His	Gly	Gly	Gly	Ile	Thr	Glu	Ala	Ala	Ala
1				5					10					15	
Arg	Tyr	Gly	Gly	Arg	Pro	Glu	Asp	Trp	Leu	Asp	Leu	Ser	Thr	Gly	Ile
		20						25					30		
Asn	Pro	Cys	Pro	Val	Ala	Leu	Pro	Ala	Val	Pro	Glu	Arg	Ala	Trp	His
		35					40					45			
Arg	Leu	Pro	Asp	Arg	Gln	Thr	Val	Asp	Asp	Ala	Arg	Ser	Ala	Ala	Ala
	50					55					60				
Asp	Tyr	Tyr	Arg	Thr	Asn	Gly	Val	Leu	Pro	Leu	Pro	Val	Pro	Gly	Thr
65					70					75					80
Gln	Ser	Val	Ile	Gln	Leu	Leu	Pro	Arg	Leu	Ala	Pro	Ala	Asn	Arg	His
			85						90					95	
Val	Ala	Ile	Phe	Gly	Pro	Thr	Tyr	Gly	Glu	Tyr	Ala	Arg	Val	Leu	Glu
			100					105					110		
Ala	Ala	Gly	Phe	Ala	Val	Asp	Arg	Val	Ala	Asp	Ala	Asp	Ala	Leu	Thr
		115					120					125			
Ala	Glu	His	Gly	Leu	Val	Ile	Val	Val	Asn	Pro	Asn	Asn	Pro	Thr	Gly
	130					135					140				
Arg	Ala	Leu	Ala	Pro	Ala	Glu	Leu	Leu	Ala	Ile	Ala	Ala	Arg	Gln	Lys
145					150					155					160
Ala	Ser	Gly	Gly	Leu	Leu	Val	Asp	Glu	Ala	Phe	Gly	Asp	Leu	Glu	
			165					170					175		
Pro	Gln	Leu	Ser	Val	Ala	Gly	His	Ala	Ser	Gly	Gln	Gly	Asn	Leu	Ile
			180					185					190		
Val	Phe	Arg	Ser	Phe	Gly	Lys	Phe	Phe	Gly	Leu	Ala	Gly	Leu	Arg	Leu
		195					200					205			
Gly	Phe	Val	Val	Ala	Thr	Glu	Pro	Val	Leu	Ala	Ser	Phe	Ala	Asp	Trp
	210					215					220				
Leu	Gly	Pro	Trp	Ala	Val	Ser	Gly	Pro	Ala	Leu	Thr	Ile	Ser	Lys	Ala
225					230					235					240
Leu	Met	Gln	Gly	Asp	Thr	Lys	Ala	Ile	Ala	Ala	Gly	Ile	Leu	Glu	Arg
				245					250					255	
Arg	Ala	Gly	Leu	Asp	Ala	Ala	Leu	Asp	Gly	Ala	Gly	Leu	Asn	Arg	Ile
			260					265					270		
Gly	Gly	Thr	Gly	Leu	Phe	Val	Leu	Val	Glu	His	Pro	Arg	Ala	Ala	Leu
		275					280					285			
Leu	Gln	Glu	Arg	Leu	Cys	Glu	Ala	His	Ile	Leu	Thr	Arg	Lys	Phe	Asp
	290					295					300				
Tyr	Ala	Pro	Thr	Trp	Leu	Arg	Val	Gly	Leu	Ala	Pro	Asp	Ala	Ala	Gly
305					310				315						320
Asp	Arg	Arg	Leu	Ala	Asp	Ala	Leu	Ala	Arg	Met	Glu	Leu			
			325						330						

(2) INFORMATION FOR SEQ ID NO: 9:

(i)

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

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- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas denitrificans*
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:
- (ix) FEATURE:
(A) NAME/KEY: cobD
(B) LOCATION: 4284-5252 bp of SEQ ID NO: 1
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GTGTCGGAGA	CGATCCTGCT	CATTCTCGCG	CTGGCGCTGG	TGATCGACCG	CGTTGTCGGC	60
GATCCGGACT	GGCTCTGGGC	GCGCGTGCCG	CATCCGGTCG	TGTTTTTCGG	CAAGGCCATC	120
GGCTTTTTTCG	ACGCGCGGCT	GAACCGGGAG	GACCTCGAGG	ATAGCGCGCG	CAAATTTTCGT	180
GGCGTCGTCG	CGATCCTTTT	GTTGCTTGGC	ATCAGCGCCT	GGTTCGGCCA	TCTGCTGCAT	240
CGCCTGTTTCG	CCGTCTCTCG	ACCGCTCGGC	TTTCTGCTCG	AGGCGGTTCT	GGTCGCGGTC	300
TTCTTGGCAC	AGAAGAGCCT	CGCCGATCAC	GTGCGTCGCG	TGGCCGGGGG	CTTGCGACAG	360
GGCGGGCTGG	AAGGCGGGCG	TGCCGCCGTG	TCGATGATCG	TTGGTCGCGA	TCCAAAGACG	420
CTCGACGAGC	CGGCGGTCTG	CCGTGCCGCG	ATCGAAAGCC	TTGCCGAGAA	TTTCTCCGAC	480
GGCGTCGTGG	CGCCGGCCTT	CTGGTACGCG	GTTGCCGGCC	TGCCGGGGCT	TCTTGCCTAC	540
AAGATGCTGA	ACACCGCCGA	TTGATGATC	GGCCACAAGT	CGCCGAAATA	TCTGCACTTC	600
GGCTGGGCCT	CGGCCCGACT	CGACGATCTC	GCCAACCTGC	CGGCAGCGAG	GCTCTCGATC	660
CTTTTGATCT	CAGCCGGTGC	GCTGATCCAT	CGTGGCGCCA	GCGCCGCCAA	GGATGCGCTG	720
ACCGTGGCCC	TTCGCGACCA	TGGCCTGCAC	CGCTCGCCGA	ACTCCGGCTG	GCCGGAAGCG	780
GCCATGGCCG	GCGCGCTCGA	TCTGCAGCTT	GCCGGTCCGC	GGATCTATGG	CGGCGTCAAG	840
GTCAGCGAAC	CTATGATCAA	CGGTCCGGGC	CGAGCGGTTG	CAACAAGCGA	AGACATCGAC	900
GCCGGTATTG	CTGTATTTTA	TGGCGCCTGT	ACGGTCATGG	CCGGGTTTGT	TCTTGCAATC	960
GCAATGATTT	GA					972

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 amino acids
(B) TYPE: Amino Acid
(C) STRANDEDNESS:
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas denitrificans*
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:

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(H) CELL LINE:
(I) ORGANELLE:

(ix) FEATURE:
(A) NAME/KEY: COBD
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Translation product of SEQ ID NO:9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Ser	Glu	Thr	Ile	Leu	Leu	Ile	Leu	Ala	Leu	Ala	Leu	Val	Ile	Asp
1				5					10					15	
Arg	Val	Val	Gly	Asp	Pro	Asp	Trp	Leu	Trp	Ala	Arg	Val	Pro	His	Pro
			20					25					30		
Val	Val	Phe	Phe	Gly	Lys	Ala	Ile	Gly	Phe	Phe	Asp	Ala	Arg	Leu	Asn
		35				40					45				
Arg	Glu	Asp	Leu	Glu	Asp	Ser	Ala	Arg	Lys	Phe	Arg	Gly	Val	Val	Ala
	50					55					60				
Ile	Leu	Leu	Leu	Leu	Gly	Ile	Ser	Ala	Trp	Phe	Gly	His	Leu	Leu	His
65					70				75					80	
Arg	Leu	Phe	Ala	Val	Leu	Gly	Pro	Leu	Gly	Phe	Leu	Leu	Glu	Ala	Val
			85					90						95	
Leu	Val	Ala	Val	Phe	Leu	Ala	Gln	Lys	Ser	Leu	Ala	Asp	His	Val	Arg
			100				105						110		
Arg	Val	Ala	Gly	Gly	Leu	Arg	Gln	Gly	Gly	Leu	Glu	Gly	Gly	Arg	Ala
		115				120						125			
Ala	Val	Ser	Met	Ile	Val	Gly	Arg	Asp	Pro	Lys	Thr	Leu	Asp	Glu	Pro
	130					135					140				
Ala	Val	Cys	Arg	Ala	Ala	Ile	Glu	Ser	Leu	Ala	Glu	Asn	Phe	Ser	Asp
145					150					155					160
Gly	Val	Val	Ala	Pro	Ala	Phe	Trp	Tyr	Ala	Val	Ala	Gly	Leu	Pro	Gly
			165					170						175	
Leu	Leu	Ala	Tyr	Lys	Met	Leu	Asn	Thr	Ala	Asp	Ser	Met	Ile	Gly	His
			180					185					190		
Lys	Ser	Pro	Lys	Tyr	Leu	His	Phe	Gly	Trp	Ala	Ser	Ala	Arg	Leu	Asp
		195					200					205			
Asp	Leu	Ala	Asn	Leu	Pro	Ala	Ala	Arg	Leu	Ser	Ile	Leu	Leu	Ile	Ser
	210					215					220				
Ala	Gly	Ala	Leu	Ile	His	Arg	Gly	Ala	Ser	Ala	Ala	Lys	Asp	Ala	Leu
225					230					235					240
Thr	Val	Ala	Leu	Arg	Asp	His	Gly	Leu	His	Arg	Ser	Pro	Asn	Ser	Gly
			245					250						255	
Trp	Pro	Glu	Ala	Ala	Met	Ala	Gly	Ala	Leu	Asp	Leu	Gln	Leu	Ala	Gly
		260					265						270		
Pro	Arg	Ile	Tyr	Gly	Gly	Val	Lys	Val	Ser	Glu	Pro	Met	Ile	Asn	Gly
		275					280					285			
Pro	Gly	Arg	Ala	Val	Ala	Thr	Ser	Glu	Asp	Ile	Asp	Ala	Gly	Ile	Ala
	290					295					300				
Val	Phe	Tyr	Gly	Ala	Cys	Thr	Val	Met	Ala	Gly	Phe	Val	Leu	Ala	Ile
305					310					315					320
Ala	Met	Ile													

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Unknown

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- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas denitrificans*
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:
- (ix) FEATURE:
(A) NAME/KEY: cobE
(B) LOCATION: 549-1011 bp of SEQ ID NO: 1
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGCCATCGG	GCCAACACTC	TGCACAGACG	ACGAAAGCAG	GAGCCGGGCT	GGTGCTCGGG	60
CTCGGCTGCG	AGCGTCGCAC	GCCGGCCGAA	GAGGTGATCG	CCCTTGCCGA	GCGTGCGCTT	120
GCCGATGCCG	GTGTTGCGCC	CGGCGATCTG	CGGCTGGTCG	CCTCGCTCGA	TGCTCGCGCC	180
GAGGAGCCGG	CGATCCTGGC	GGCCGCTCAG	CATTTGCGGG	TTCCGGCCGC	GTTCTACGAT	240
GCCGCCACGC	TGAAGCCGA	AGCTTCCCGG	CTCGCCAACC	CGTCCGAGAT	CGTCTTTGCC	300
TACACGGGTT	GTCATGGCGT	TGCCGAGGGT	GCAGCGCTCG	TCGGCGCCGG	TCGCGAAGCC	360
GTGCTGATTG	TGCAGAAGAT	CGTCTCCGCC	CATGCGACGG	CCGCACTTGC	CGGGCCGGCG	420
ACCTTGCGCG	CCGAAAAGCG	CATCCAGGCG	GCGGAGGCTG	TCTGA		465

- (2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 amino acids
(B) TYPE: Amino Acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas denitrificans*
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:
- (ix) FEATURE:
(A) NAME/KEY: COBE
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Translation product of SEQ ID NO:11

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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Met Pro Ser Gly Gln His Ser Ala Gln Thr Thr Lys Ala Gly Ala Gly
1      5      10      15
Leu Val Leu Gly Leu Gly Cys Glu Arg Arg Thr Pro Ala Glu Glu Val
20     25     30
Ile Ala Leu Ala Glu Arg Ala Leu Ala Asp Ala Gly Val Ala Pro Gly
35     40     45
Asp Leu Arg Leu Val Ala Ser Leu Asp Ala Arg Ala Glu Glu Pro Ala
50     55     60
Ile Leu Ala Ala Ala Gln His Phe Ala Val Pro Ala Ala Phe Tyr Asp
65     70     75     80
Ala Ala Thr Leu Glu Ala Glu Ala Ser Arg Leu Ala Asn Pro Ser Glu
85     90     95
Ile Val Phe Ala Tyr Thr Gly Cys His Gly Val Ala Glu Gly Ala Ala
100    105    110
Leu Val Gly Ala Gly Arg Glu Ala Val Leu Ile Val Gln Lys Ile Val
115    120    125
Ser Ala His Ala Thr Ala Ala Leu Ala Gly Pro Ala Thr Leu Arg Ala
130    135    140
Glu Lys Arg Ile Gln Ala Ala Glu Ala Val
145    150

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(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 786 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 - (A) ORGANISM: Pseudomonas denitrificans
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (ix) FEATURE:
 - (A) NAME/KEY: cobF
 - (B) LOCATION: 736-1521 bp of SEQ ID NO: 2
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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ATGGCGGAGG CGGGCATGCG CAAAATTCTG ATCATCGGCA TCGGTTTCGGG CAATCCCGAA      60
CACATGACCG TGCAGGCGAT CAACGCGCTG AACTGCGCCG ACGTGCTCTT TATCCCGACC      120
AAGGGAGCGA AGAAGACCGA GCTTGCCGAA GTGCGCCGCG ACATCTGCGC CCGCTACGTC      180
ACGCGCAAGG ACAGCCGCAC CGTCGAGTTC GCGGTGCCCG TGCGGCGCAC CGAAGGCGTC      240
AGCTATGACG GCAGCGTCGA TGA CTGGCAC GCCCAGATCG CTGGGATTTA CGAAGCGCTT      300
CTATCGAAGG AGTTGGGCGA AGAGGGAAC TGGCGCTTTC TCGTCTGGGG CGACCCGATG      360
CTCTATGACA GCACCATTCG CATCGTCGAG CGGGTCAAGG CACGCGGTGA GGTGCGCTTC      420

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GCCTACGACG	TCATTCCCGG	GATCACCAGT	CTGCAGGCGC	TTTGCGCCAG	CCACCGCATT	480
CCGCTGAACC	TCGTCGGCAA	GCCGGTGGAG	ATCACCACGG	GGCGTCGGCT	GCACGAAAGC	540
TTTCCCGAGA	AGAGCCAGAC	CTCGGTCGTC	ATGCTCGATG	GCGAACAGGC	GTTTCAGCGG	600
GTCGAGGACC	CGGAGGCGGA	GATCTATTGG	GGCGCCTATC	TCGGCACGCG	GGATGAGATC	660
GTCATTTCCG	GCCGCGTGGC	TGAGGTGAAG	GACCGGATCC	TTGAAACGCG	GGCGGCGGCG	720
CGCGCGAAGA	TGGGATGGAT	CATGGACATC	TATCTCTGTC	GCAAGGGCGC	CGACTTCGAC	780
GAGTGA						786

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 amino acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas denitrificans*
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (ix) FEATURE:
 - (A) NAME/KEY: COBF
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION: Translation product of SEQ ID NO:13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met	Ala	Glu	Ala	Gly	Met	Arg	Lys	Ile	Leu	Ile	Ile	Gly	Ile	Gly	Ser
1				5					10					15	
Gly	Asn	Pro	Glu	His	Met	Thr	Val	Gln	Ala	Ile	Asn	Ala	Leu	Asn	Cys
			20					25					30		
Ala	Asp	Val	Leu	Phe	Ile	Pro	Thr	Lys	Gly	Ala	Lys	Lys	Thr	Glu	Leu
		35					40					45			
Ala	Glu	Val	Arg	Arg	Asp	Ile	Cys	Ala	Arg	Tyr	Val	Thr	Arg	Lys	Asp
	50				55				60						
Ser	Arg	Thr	Val	Glu	Phe	Ala	Val	Pro	Val	Arg	Thr	Glu	Gly	Val	
65				70				75					80		
Ser	Tyr	Asp	Gly	Ser	Val	Asp	Asp	Trp	His	Ala	Gln	Ile	Ala	Gly	Ile
		85						90					95		
Tyr	Glu	Ala	Leu	Leu	Ser	Lys	Glu	Leu	Gly	Glu	Glu	Gly	Thr	Gly	Ala
		100					105					110			
Phe	Leu	Val	Trp	Gly	Asp	Pro	Met	Leu	Tyr	Asp	Ser	Thr	Ile	Arg	Ile
		115				120					125				
Val	Glu	Arg	Val	Lys	Ala	Arg	Gly	Glu	Val	Ala	Phe	Ala	Tyr	Asp	Val
	130					135				140					
Ile	Pro	Gly	Ile	Thr	Ser	Leu	Gln	Ala	Leu	Cys	Ala	Ser	His	Arg	Ile
145				150				155					160		
Pro	Leu	Asn	Leu	Val	Gly	Lys	Pro	Val	Glu	Ile	Thr	Thr	Gly	Arg	Arg
		165						170					175		
Leu	His	Glu	Ser	Phe	Pro	Glu	Lys	Ser	Gln	Thr	Ser	Val	Val	Met	Leu

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Asp	Gly	Glu	180	Gln	Ala	Phe	Gln	Arg	185	Val	Glu	Asp	Pro	Glu	190	Ala	Glu	Ile
		195						200						205				
Tyr	Trp	Gly	Ala	Tyr	Leu	Gly	Thr	Arg	Asp	Glu	Ile	Val	Ile	Ser	Gly			
	210					215				220								
Arg	Val	Ala	Glu	Val	Lys	Asp	Arg	Ile	Leu	Glu	Thr	Arg	Ala	Ala	Ala			
225					230					235					240			
Arg	Ala	Lys	Met	Gly	Trp	Ile	Met	Asp	Ile	Tyr	Leu	Leu	Arg	Lys	Gly			
			245						250					255				
Ala	Asp	Phe	Asp	Glu														
			260															

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1380 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 (A) ORGANISM: *Pseudomonas denitrificans*
 (B) STRAIN:
 (C) INDIVIDUAL ISOLATE:
 (D) DEVELOPMENTAL STAGE:
 (E) HAPLOTYPE:
 (F) TISSUE TYPE:
 (G) CELL TYPE:
 (H) CELL LINE:
 (I) ORGANELLE:
- (ix) FEATURE:
 (A) NAME/KEY: cobG
 (B) LOCATION: 1620-2999 bp of SEQ ID NO: 2
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATGACGGATT	TGATGACCAG	CTGCGCCCTT	CCATTGACCG	GAGATGCCGG	CACCGTCGCT	60
TCGATGCGCC	GCGGCGCCTG	CCCGTCCTTG	GCAGAGCCGA	TGCAGACCGG	CGACGGCCTG	120
CTCGTGAGGG	TGAGGCCAAC	GGATGACAGC	CTGACGCTGC	CGAAGGTCAT	TGCCCTTGCC	180
ACGGCTGCCG	AGCGCTTCGG	CAATGGCATC	ATCGAGATTA	CCGCGCGCGG	AAACCTGCAG	240
CTTCGCGGCC	TGAGCGCGGC	TTCGGTGCCA	AGGCTGGCGC	AGGCGATCGG	CGATGCGGAG	300
ATCGCCATTG	CCGAGGGGCT	CGCGATCGAG	GTGCCGCCCC	TGGCCGGCAT	CGACCCGGAC	360
GAGATCGCCG	ATCCGCGGCC	GATTGCCACT	GAGCTTCGTG	AAGCGTTGGA	TGTGCGCCAG	420
GTGCCGTTGA	AGCTTGACCC	CAAATTATCC	GTCGTCATCG	ATAGCGGTGG	CCGGTTTGGT	480
CTCGGCGCTG	TCGTCGCCGA	CATTGCGCTT	CAGGCGGTTT	CGACTGTCGC	GGGGGTGGCC	540
TGGGTGCTGT	CGCTTGCGCG	CACGTCAACG	AAGGCATCGA	GCGTCGGGAC	GTTGGCCGGC	600
AACGCGGTG	TGCCGGCCCT	GATCACCATT	CTCGAGAAAC	TGGCGAGCCT	GGGCACGACG	660
ATGCGCGGGC	CGGATCTGGA	CCCGTCGGAA	ATCCGCGCGC	TCTGTCGCTG	TGAGACATCG	720
TCCGAACGCC	CGGCCGCTCC	GCGTTCGGCC	GCAATACCCG	GCATTCATGC	GCTGGGTAAAC	780
GCCGACACCG	TTCTCGGCCT	CGGTCTGGCC	TTTGCTCAGG	TGGAGGCCGC	CGCGCTGGCA	840
TCCTACCTGC	ATCAGGTCCA	GGCGCTTGCC	GCCAATGCGA	TCCGGCTTGC	GCCCCGGCAC	900
GCCTTCTTCG	TCCTCGGCCT	TTGCCCCGAG	ACCGCGGCTG	TGGCGCAGAG	CCTGGCAGCG	960
TCACACGGTT	TTGCGATTGC	CGAGCAGGAT	CCGCGCAATG	CGATCGCCAC	CTGCGCCGGC	1020
AGCAAGGGTT	GCGCCTCGGC	GTGGATGGAA	ACCAAGGGCA	TGGCCGAGCG	CCTCGTCGAG	1080

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ACGGCGCCGG	AATTGCTCGA	CGGGTCGCTC	ACCGTGCATC	TCTCCGGCTG	CGCCAAGGGC	1140
TGCGCCCGGC	CGAAGCCGTC	CGAACTGACG	CTTGTCCGGT	CGCCATCAGG	ATACGGGCTT	1200
GTCGTAAATG	GGGCTGCCAA	TGGCTTGCCA	AGCGCTACA	CCGATGAGAA	TGGAATGGGA	1260
TCCGCCCTTG	CCCGGCTCGG	CCGGCTGGTG	CGGCAAAACA	AAGACGCTGG	CGAATCGGCG	1320
CAGTCCTGTC	TTACACGGCT	CGGAGCTGCG	CGCGTCTCGG	CAGCGTTCGA	ACAGGGATAG	1380

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 459 amino acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas denitrificans*
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (ix) FEATURE:
 - (A) NAME/KEY: COBG
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION: Translation product of SEQ ID NO:15
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met	Thr	Asp	Leu	Met	Thr	Ser	Cys	Ala	Leu	Pro	Leu	Thr	Gly	Asp	Ala
1				5					10					15	
Gly	Thr	Val	Ala	Ser	Met	Arg	Arg	Gly	Ala	Cys	Pro	Ser	Leu	Ala	Glu
			20					25					30		
Pro	Met	Gln	Thr	Gly	Asp	Gly	Leu	Leu	Val	Arg	Val	Arg	Pro	Thr	Asp
		35				40					45				
Asp	Ser	Leu	Thr	Leu	Pro	Lys	Val	Ile	Ala	Leu	Ala	Thr	Ala	Ala	Glu
	50					55				60					
Arg	Phe	Gly	Asn	Gly	Ile	Ile	Glu	Ile	Thr	Ala	Arg	Gly	Asn	Leu	Gln
65					70					75				80	
Leu	Arg	Gly	Leu	Ser	Ala	Ala	Ser	Val	Pro	Arg	Leu	Ala	Gln	Ala	Ile
			85					90					95		
Gly	Asp	Ala	Glu	Ile	Ala	Ile	Ala	Glu	Gly	Leu	Ala	Ile	Glu	Val	Pro
		100						105					110		
Pro	Leu	Ala	Gly	Ile	Asp	Pro	Asp	Glu	Ile	Ala	Asp	Pro	Arg	Pro	Ile
		115				120					125				
Ala	Thr	Glu	Leu	Arg	Glu	Ala	Leu	Asp	Val	Arg	Gln	Val	Pro	Leu	Lys
	130					135				140					
Leu	Ala	Pro	Lys	Leu	Ser	Val	Val	Ile	Asp	Ser	Gly	Gly	Arg	Phe	Gly
145				150					155					160	
Leu	Gly	Ala	Val	Val	Ala	Asp	Ile	Arg	Leu	Gln	Ala	Val	Ser	Thr	Val
		165						170					175		
Ala	Gly	Val	Ala	Trp	Val	Leu	Ser	Leu	Gly	Gly	Thr	Ser	Thr	Lys	Ala
		180						185					190		
Ser	Ser	Val	Gly	Thr	Leu	Ala	Gly	Asn	Ala	Val	Val	Pro	Ala	Leu	Ile

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Thr	Ile	195	Leu	Glu	Lys	Leu	Ala	200	Ser	Leu	Gly	Thr	Thr	205	Met	Arg	Gly	Arg
210	215												220					
Asp	Leu	225	Asp	Pro	Ser	Glu	Ile	230	Arg	Ala	Leu	Cys	Arg	235	Cys	Glu	Thr	Ser
240																		
Ser	Glu	245	Arg	Pro	Ala	Ala	Pro	250	Arg	Ser	Ala	Ala	Ile	255	Pro	Gly	Ile	His
260																		
Ala	Leu	265	Gly	Asn	Ala	Asp	Thr	270	Val	Leu	Gly	Leu	Gly	275	Leu	Ala	Phe	Ala
280																		
Gln	Val	285	Glu	Ala	Ala	Ala	Leu	290	Ala	Ser	Tyr	Leu	His	295	Gln	Val	Gln	Ala
300																		
Leu	Gly	305	Ala	Asn	Ala	Ile	Arg	310	Leu	Ala	Pro	Gly	His	315	Ala	Phe	Phe	Val
320																		
Leu	Gly	325	Leu	Cys	Pro	Glu	Thr	330	Ala	Ala	Val	Ala	Gln	335	Ser	Leu	Ala	Ala
340																		
Ser	His	345	Gly	Phe	Arg	Ile	Ala	350	Glu	Gln	Asp	Pro	Arg	355	Asn	Ala	Ile	Ala
360																		
Thr	Cys	365	Ala	Gly	Ser	Lys	Gly	370	Cys	Ala	Ser	Ala	Trp	375	Met	Glu	Thr	Lys
380																		
Gly	Met	385	Ala	Glu	Arg	Leu	Val	390	Glu	Thr	Ala	Pro	Glu	395	Leu	Leu	Asp	Gly
400																		
Ser	Leu	405	Thr	Val	His	Leu	Ser	410	Gly	Cys	Ala	Lys	Gly	415	Cys	Ala	Arg	Pro
420																		
Lys	Pro	425	Ser	Glu	Leu	Thr	Leu	430	Val	Gly	Ala	Pro	Ser	435	Gly	Tyr	Gly	Leu
440																		
Val	Val	445	Asn	Gly	Ala	Asn	Gly	450	Leu	Pro	Ser	Ala	Tyr	455	Thr	Asp	Glu	
460																		
Asn	Gly	465	Met	Gly	Ser	Ala	Leu	470	Ala	Arg	Leu	Gly	Arg	475	Leu	Val	Arg	Gln
480																		
Asn	Lys	485	Asp	Ala	Gly	Glu	Ser	490	Ala	Gln	Ser	Cys	Leu	495	Thr	Arg	Leu	Gly
500																		
Ala	Ala	505	Arg	Val	Ser	Ala	Ala	510	Phe	Glu	Gln	Gly						

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas denitrificans*
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (ix) FEATURE:
 - (A) NAME/KEY: cobH
 - (B) LOCATION: 3002-3634 bp of SEQ ID NO: 2
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATGCCTGAGT	ATGATTACAT	TCGCGATGGC	AACGCCATCT	ACGAGCGTTC	CTTCGCCATC	60
ATCCGCGCCG	AGGCCGATCT	GTCGCGCTTC	TCCGAAGAGG	AAGCGGATCT	GGCTGTGCGC	120
ATGGTGCACG	CCTGCGGTTT	CGTCGAGGCG	ACCAGGCAGT	TCGTGTTTTT	TCCCGATTTC	180
GTAAGCTCGG	CCCGTGCGGC	GCTGAAAGCC	GGTGCGCCGA	TCCTCTGCGA	TGCCGAGATG	240
GTTGCGCACG	GTGTCACCCG	CGCCCGTCTG	CCGGCCGGCA	ACGAGGTGAT	CTGCACGCTG	300
CGCGATCCTC	GCACGCCCGC	ACTTGCGGCC	GAGATCGGCA	ACACCCGCTC	CGCCGCAGCC	360
CTGAAGCTCT	GGAGCGAGCG	GCTGGCCGGT	TCGGTGGTCG	CGATCGGCAA	CGCGCCGACG	420
GCGTTGTTCT	TCCTCTTGGA	AATGCTGCGC	GACGGCGCGC	CGAAGCCGGC	GGCAATCCTC	480
GGCATGCCCC	TCGGTTTCGT	CGGTGCGGCG	GAATCGAAGG	ATGCGCTGGC	CGAGAACTCC	540
TATGGCGTTC	CCTTCGCCAT	CGTGCGCGGC	CGCCTCGGCG	GGAGTGCCAT	GACGGCGGCA	600
GCGCTTAACT	CGCTCGCGAG	GCCGGGCCTG	TGA			633

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 amino acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas denitrificans*
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (ix) FEATURE:
 - (A) NAME/KEY: COBH
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION: Translation product of SEQ ID NO:17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met	Pro	Glu	Tyr	Asp	Tyr	Ile	Arg	Asp	Gly	Asn	Ala	Ile	Tyr	Glu	Arg	1	5	10	15
Ser	Phe	Ala	Ile	Ile	Arg	Ala	Glu	Ala	Asp	Leu	Ser	Arg	Phe	Ser	Glu	20	25	30	
Glu	Glu	Ala	Asp	Leu	Ala	Val	Arg	Met	Val	His	Ala	Cys	Gly	Ser	Val	35	40	45	
Glu	Ala	Thr	Arg	Gln	Phe	Val	Phe	Ser	Pro	Asp	Phe	Val	Ser	Ser	Ala	50	55	60	
Arg	Ala	Ala	Leu	Lys	Ala	Gly	Ala	Pro	Ile	Leu	Cys	Asp	Ala	Glu	Met	65	70	75	80
Val	Ala	His	Gly	Val	Thr	Arg	Ala	Arg	Leu	Pro	Ala	Gly	Asn	Glu	Val	85	90	95	
Ile	Cys	Thr	Leu	Arg	Asp	Pro	Arg	Thr	Pro	Ala	Leu	Ala	Ala	Glu	Ile	100	105	110	
Gly	Asn	Thr	Arg	Ser	Ala	Ala	Ala	Leu	Lys	Leu	Trp	Ser	Glu	Arg	Leu	115	120	125	
Ala	Gly	Ser	Val	Val	Ala	Ile	Gly	Asn	Ala	Pro	Thr	Ala	Leu	Phe	Phe				

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130	135	140
Leu Leu Glu Met Leu Arg Asp Gly Ala Pro Lys Pro Ala Ala Ile Leu		
145	150	155
Gly Met Pro Val Gly Phe Val Gly Ala Ala Glu Ser Lys Asp Ala Leu		
165	170	175
Ala Glu Asn Ser Tyr Gly Val Pro Phe Ala Ile Val Arg Gly Arg Leu		
180	185	190
Gly Gly Ser Ala Met Thr Ala Ala Leu Asn Ser Leu Ala Arg Pro		
195	200	205
Gly Leu		
210		

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 738 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas denitrificans*
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (ix) FEATURE:
 - (A) NAME/KEY: *cobI*
 - (B) LOCATION: 3631-4368 bp of SEQ ID NO: 2
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 19:	
GTGAGCGGCG	TCGGCGTGGG	60
CTTTTGACGG	TCAAGGCGGT	120
AAGGCCGGGC	GAAGCGGTAA	180
GTCGAGCTGC	CGCTATACTA	240
AAGACCCAGA	TCACCGACTT	300
GCCGGGCGCA	CGGTCGCCGT	360
CATCTGCATG	TGCGGCTCGC	420
ATGTCCGGCT	GTTGGTCGCT	480
GTGCTTCCGG	GCACCATGGC	540
GCCGTGATCA	TGAAGGTCGG	600
GGCCGTCTCG	ACCAGGCCGT	660
GCTCTTGCGG	AAAAGGCCGA	720
TGGAAGGACC	GACCATGA	738

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 245 amino acids
 - (B) TYPE: Amino Acid

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(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:
(A) ORGANISM: Pseudomonas denitrificans
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(ix) FEATURE:
(A) NAME/KEY: COBI
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Translation product of SEQ ID NO:19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```
Met Ser Gly Val Gly Val Gly Arg Leu Ile Gly Val Gly Thr Gly Pro
1      5      10      15
Gly Asp Pro Glu Leu Leu Thr Val Lys Ala Val Lys Ala Leu Gly Gln
20      25      30
Ala Asp Val Leu Ala Tyr Phe Ala Lys Ala Gly Arg Ser Gly Asn Gly
35      40      45
Arg Ala Val Val Glu Gly Leu Leu Lys Pro Asp Leu Val Glu Leu Pro
50      55      60
Leu Tyr Tyr Pro Val Thr Thr Glu Ile Asp Lys Asp Asp Gly Ala Tyr
65      70      75      80
Lys Thr Gln Ile Thr Asp Phe Tyr Asn Ala Ser Ala Glu Ala Val Ala
85      90      95
Ala His Leu Ala Ala Gly Arg Thr Val Ala Val Leu Ser Glu Gly Asp
100     105     110
Pro Leu Phe Tyr Gly Ser Tyr Met His Leu His Val Arg Leu Ala Asn
115     120     125
Arg Phe Pro Val Glu Val Ile Pro Gly Ile Thr Ala Met Ser Gly Cys
130     135     140
Trp Ser Leu Ala Gly Leu Pro Leu Val Gln Gly Asp Asp Val Leu Ser
145     150     155     160
Val Leu Pro Gly Thr Met Ala Glu Ala Glu Leu Gly Arg Arg Leu Ala
165     170     175
Asp Thr Glu Ala Ala Val Ile Met Lys Val Gly Arg Asn Leu Pro Lys
180     185     190
Ile Arg Arg Ala Leu Ala Ala Ser Gly Arg Leu Asp Gln Ala Val Tyr
195     200     205
Val Glu Arg Gly Thr Met Lys Asn Ala Ala Met Thr Ala Leu Ala Glu
210     215     220
Lys Ala Asp Asp Glu Ala Pro Tyr Phe Ser Leu Val Leu Val Pro Gly
225     230     235     240
Trp Lys Asp Arg Pro
245
```

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 764 base pairs

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- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: *cobJ*
- (B) LOCATION: 4365-5129 bp of SEQ ID NO: 2
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATGACCGGTA	CGCTCTATGT	CGTCGGTACC	GGACCGGGCA	GCGCCAAGCA	GATGACGCCG	60
GAAACGGCGG	AAGCCGTTGC	GGCCGCTCAG	GAGTTTTACG	GCTACTTTCC	CTATCTCGAC	120
CGGCTGAACC	TCAGACCGGA	TCAGATCCGT	GTCGCCTCGG	ACAACCGCGA	GGAGCTCGAT	180
CGGGCACAGG	TCGCGCTGAC	GCGGGCTGCG	GCAGGCGTGA	AGGTCTGCAT	GGTCTCCGGT	240
GGCGATCCCG	GTGTCTTTGC	CATGGCGGCC	GCCGTCTGCG	AGGCGATCGA	CAAGGGACCG	300
GCGGAATGGA	AGTCGGTTGA	ACTGGTGATC	ACGCCCGGCG	TGACCGCGAT	GCTCGCCGTT	360
GCCGCCCGCA	TCGGCGCGCC	GCTCGGTCAT	GATTTCTGTG	CGATCTCGCT	TTCCGACAAT	420
CTGAAGCCCT	GGGAAGTCAT	CACCCGGCGT	CTCAGGCTGG	CGGCGGAAGC	GGGCTTCGTC	480
ATTGCCCTCT	ACAATCCGAT	CAGCAAGGCG	CGGCCCTGGC	AGCTCGGTGA	GGCCTTCGAG	540
CTTCTGCGCA	GCGTTCTGCC	GGCAAGCGTT	CCGGTCATCT	TCGGCCGTGC	GGCCGGGCGG	600
CCGGACGAAC	GGATCGCGGT	GATGCCGCTC	GGCGAGGCCG	ATGCCAACCG	CGCCGACATG	660
GCGACCTGCG	TCATCATCGG	CTCGCCGGAG	ACGCGCATCG	TCGAGCGCGA	CGGCCAACCC	720
GATCTCGTCT	ACACACCGCG	CTTCTATGCA	GGGGCGAGCC	AGTG		764

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

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- (ix) FEATURE:
(A) NAME/KEY: COBJ
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Translation product of SEQ ID NO:21
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```
Met Thr Gly Thr Leu Tyr Val Val Gly Thr Gly Pro Gly Ser Ala Lys
1      5      10      15
Gln Met Thr Pro Glu Thr Ala Glu Ala Val Ala Ala Ala Gln Glu Phe
20      25      30
Tyr Gly Tyr Phe Pro Tyr Leu Asp Arg Leu Asn Leu Arg Pro Asp Gln
35      40      45
Ile Arg Val Ala Ser Asp Asn Arg Glu Glu Leu Asp Arg Ala Gln Val
50      55      60
Ala Leu Thr Arg Ala Ala Ala Gly Val Lys Val Cys Met Val Ser Gly
65      70      75      80
Gly Asp Pro Gly Val Phe Ala Met Ala Ala Val Cys Glu Ala Ile
85      90      95
Asp Lys Gly Pro Ala Glu Trp Lys Ser Val Glu Leu Val Ile Thr Pro
100     105     110
Gly Val Thr Ala Met Leu Ala Val Ala Ala Arg Ile Gly Ala Pro Leu
115     120     125
Gly His Asp Phe Cys Ala Ile Ser Leu Ser Asp Asn Leu Lys Pro Trp
130     135     140
Glu Val Ile Thr Arg Arg Leu Arg Leu Ala Ala Glu Ala Gly Phe Val
145     150     155     160
Ile Ala Leu Tyr Asn Pro Ile Ser Lys Ala Arg Pro Trp Gln Leu Gly
165     170     175
Glu Ala Phe Glu Leu Leu Arg Ser Val Leu Pro Ala Ser Val Pro Val
180     185     190
Ile Phe Gly Arg Ala Ala Gly Arg Pro Asp Glu Arg Ile Ala Val Met
195     200     205
Pro Leu Gly Glu Ala Asp Ala Asn Arg Ala Asp Met Ala Thr Cys Val
210     215     220
Ile Ile Gly Ser Pro Glu Thr Arg Ile Val Glu Arg Asp Gly Gln Pro
225     230     235     240
Asp Leu Val Tyr Thr Pro Arg Phe Tyr Ala Gly Ala Ser Gln
245     250
```

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 786 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
(A) ORGANISM: Pseudomonas denitrificans
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:

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(I) ORGANELLE:

(ix)

FEATURE:

- (A) NAME/KEY: cobK
- (B) LOCATION: compl. strand of 2861-3634 bp of SEQ ID NO:2
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATGGCGGGTT	CGCTGTTCTGA	CACGTCAGCC	ATGGAAAAAC	CTCGTATTCT	GATTCTGGGT	60
GGCACCACCG	AGGCACGCGA	ACTCGCGCGC	CGCTTGCCCG	AAGATGTCCG	CTACGACACC	120
GCCATCTCGC	TGGCCGGCCG	CACCGCGGAC	CCGCGGCCCG	AGCCGGTCAA	GACGCGCATC	180
GGCGGCTTTG	GCGGCGCCGA	TGGGCTGGCG	CATTTCTGTC	ATGACGAAAA	CATCGCGCTG	240
CTGGTCGATG	CGACGCACCC	CTTTGCCGCA	CGCATTTTCG	ACAACGCCGC	GGACGCAGCG	300
CAAAGAACCG	GCGTTGCGCT	TATCGCCCTC	CGCCGACCGG	AATGGGTGCC	CCTGCCTGGC	360
GACCGCTGGA	CTGCTGTCGA	TAGCGTTGTC	GAGGCCGTCA	GCGCGCTCGG	TGATCGGCCA	420
CGCCGCGTCT	TCCTGGCGAT	AGGTCGACAG	GAAGCTTTCC	ACTTCGAGGT	CGCGCCGCAG	480
CACAGCTACG	TCATCCGCAG	CGTCGATCCG	GTGACGCCGC	CGCTTAATCT	GCCCCGACCAG	540
GAGGCGATCC	TGGCGACCGG	TCCCTTTGCG	GAAGCCGACG	AAGCCGCGTT	GCTCAGGAGT	600
CGGCAGATCG	ATGTGATCGT	CGCCAAGAAC	AGCGGTGGCA	GCGCCACCTA	CGGCAAGATT	660
GCCGCAGCGC	GCCGGCTCGG	CATCGAGGTG	ATCATGGTCG	AGCGGCGCAA	GCCCGCGGAC	720
GTGCCGACGG	TCGGCAGTTG	CGACGAGGCA	CTCAACCGCA	TCGCTCACTG	GCTCGCCCCCT	780
GCATGA						786

(2) INFORMATION FOR SEQ ID NO: 24:

(i)

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii)

MOLECULE TYPE: protein

(iii)

HYPOTHETICAL: No

(iv)

ORIGINAL SOURCE:

- (A) ORGANISM: Pseudomonas denitrificans
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix)

FEATURE:

- (A) NAME/KEY: COBK
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:23

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met	Ala	Gly	Ser	Leu	Phe	Asp	Thr	Ser	Ala	Met	Glu	Lys	Pro	Arg	Ile
1				5					10					15	
Leu	Ile	Leu	Gly	Gly	Thr	Thr	Glu	Ala	Arg	Glu	Leu	Ala	Arg	Arg	Leu
		20					25				30				
Ala	Glu	Asp	Val	Arg	Tyr	Asp	Thr	Ala	Ile	Ser	Leu	Ala	Gly	Arg	Thr
		35				40						45			

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Ala	Asp	Pro	Arg	Pro	Gln	Pro	Val	Lys	Thr	Arg	Ile	Gly	Gly	Phe	Gly
50						55					60				
Gly	Ala	Asp	Gly	Leu	Ala	His	Phe	Val	His	Asp	Glu	Asn	Ile	Ala	Leu
65				70					75						80
Leu	Val	Asp	Ala	Thr	His	Pro	Phe	Ala	Ala	Arg	Ile	Ser	His	Asn	Ala
			85					90						95	
Ala	Asp	Ala	Ala	Gln	Arg	Thr	Gly	Val	Ala	Leu	Ile	Ala	Leu	Arg	Arg
			100				105						110		
Pro	Glu	Trp	Val	Pro	Leu	Pro	Gly	Asp	Arg	Trp	Thr	Ala	Val	Asp	Ser
		115					120					125			
Val	Val	Glu	Ala	Val	Ser	Ala	Leu	Gly	Asp	Arg	Arg	Arg	Arg	Val	Phe
	130				135					140					
Leu	Ala	Ile	Gly	Arg	Gln	Glu	Ala	Phe	His	Phe	Glu	Val	Ala	Pro	Gln
145					150				155						160
His	Ser	Tyr	Val	Ile	Arg	Ser	Val	Asp	Pro	Val	Thr	Pro	Pro	Leu	Asn
			165					170						175	
Leu	Pro	Asp	Gln	Glu	Ala	Ile	Leu	Ala	Thr	Gly	Pro	Phe	Ala	Glu	Ala
			180				185						190		
Asp	Glu	Ala	Ala	Leu	Leu	Arg	Ser	Arg	Gln	Ile	Asp	Val	Ile	Val	Ala
		195					200					205			
Lys	Asn	Ser	Gly	Gly	Ser	Ala	Thr	Tyr	Gly	Lys	Ile	Ala	Ala	Ala	Arg
	210				215					220					
Arg	Leu	Gly	Ile	Glu	Val	Ile	Met	Val	Glu	Arg	Arg	Lys	Pro	Ala	Asp
225					230				235					240	
Val	Pro	Thr	Val	Gly	Ser	Cys	Asp	Glu	Ala	Leu	Asn	Arg	Ile	Ala	His
			245					250						255	
Trp	Leu	Ala	Pro	Ala											
			260												

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1242 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas denitrificans*
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (ix) FEATURE:
 - (A) NAME/KEY: *cobL*
 - (B) LOCATION: 5862-7103 bp of SEQ ID NO: 2
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

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ATGGCTGACG	TGTCGAACAG	CGAACCCGCC	ATAGTCTCCC	CCTGGCTGAC	CGTCATCGGT	60
ATCGGTGAGG	ATGGTGTAGC	GGGTCTCGGC	GACGAGGCCA	AGCGGCTGAT	CGCCGAAGCG	120
CCGGTCGTCT	ACGGCGGCCA	TCGTCACTCTG	GAGCTCGCCG	CCTCCCTCAT	CACCGGCGAA	180
GCGCACAATT	GGCTAAGCCC	CCTCGAACGC	TCGGTCGTCTG	AGATCGTCGC	GCGTCGCGGC	240
AGCCCGGTGG	TGGTGCTTGC	CTCGGGCGAC	CCGTTCTTCT	TCGGCGTCGG	CGTGACGCTG	300
GCGCGCCGCA	TCGCCTCGGC	CGAAATACGC	ACGCTTCCGG	CGCCGTCGTC	GATCAGTCTT	360
GCCGCCTCGC	GCCTCGGCTG	GGCGCTGCAG	GATGCGACGC	TCGTCTCCGT	ACATGGGCGG	420
CCGCTGGATC	TGGTGCGACC	GCATTTGCAT	CCGGGGGCGC	GTGTGCTTAC	GCTCACGTCG	480
GACGGTGCGG	GTCCGCGAGA	CCTTGCCGAG	CTTCTGGTTT	CAAGCGGCTT	CGGTCAGTCG	540
CGACTGACCG	TGCTCGAAGC	GCTGGGCGGC	GCCGGCGAAC	GGGTGACGAC	GCAGATCGCC	600
GCGCGCTTCA	TGCTCGGCCT	CGTGCATCCT	TTGAACGTCT	GCGCCATTGA	GGTGGCGGCC	660
GACGAGGGCG	CGCGCATCCT	GCCGCTTGCC	GCCGGCCGCG	ACGATGCGCT	GTTCGAACAT	720
GACGGGCAGA	TCACCAAGCG	CGAGGTGCGG	GCGCTGACGC	TGTCGGCACT	CGCACC GCGC	780
AAGGGCGAAC	TGCTATGGGA	CATCGGCGGC	GGCTCCGGCT	CGATCGGCAT	CGAATGGATG	840
CTCGCCGATC	CGACCATGCA	GGCGATCACC	ATCGAGGTTG	AGCCGGAGCG	GGCAGCGCGC	900
ATCGGCCGCA	ACGCGACGAT	GTTCGGCGTG	CCCGGGCTGA	CGGTTGTCGA	AGGCGAGGCG	960
CCGGCGGGCG	TTGCCGGCCT	GCCACAACCG	GACGCGATCT	TCATCGGCGG	CGGCGGCAGC	1020
GAAGACGGCG	TCATGGAAGC	AGCGATCGAG	GCGCTCAAGT	CAGGCGGACG	GCTGGTTGCC	1080
AACGCGGTGA	CGACGGACAT	GGAAGCGGTG	CTGCTCGATC	ATCACGCGCG	GCTCGGCGGT	1140
TCGCTGATCC	GCATCGATAT	CGCGCGTGCA	GGACCCATCG	GCGGCATGAC	CGGCTGGAAG	1200
CCGGCCATGC	CGGTCACCCA	ATGGTCGTGG	ACGAAGGGCT	AA		1242

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 413 amino acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 - (A) ORGANISM: Pseudomonas denitrificans
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (ix) FEATURE:
 - (A) NAME/KEY: COBL
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION: Translation product of SEQ ID NO:25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met	Ala	Asp	Val	Ser	Asn	Ser	Glu	Pro	Ala	Ile	Val	Ser	Pro	Trp	Leu
1				5				10						15	
Thr	Val	Ile	Gly	Ile	Gly	Glu	Asp	Gly	Val	Ala	Gly	Leu	Gly	Asp	Glu
			20					25						30	
Ala	Lys	Arg	Leu	Ile	Ala	Glu	Ala	Pro	Val	Val	Tyr	Gly	Gly	His	Arg
		35					40					45			
His	Leu	Glu	Leu	Ala	Ala	Ser	Leu	Ile	Thr	Gly	Glu	Ala	His	Asn	Trp
	50					55					60				

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Leu	Ser	Pro	Leu	Glu	Arg	Ser	Val	Val	Glu	Ile	Val	Ala	Arg	Arg	Gly
65					70				75						80
Ser	Pro	Val	Val	Val	Leu	Ala	Ser	Gly	Asp	Pro	Phe	Phe	Phe	Gly	Val
				85					90					95	
Gly	Val	Thr	Leu	Ala	Arg	Arg	Ile	Ala	Ser	Ala	Glu	Ile	Arg	Thr	Leu
			100					105					110		
Pro	Ala	Pro	Ser	Ser	Ile	Ser	Leu	Ala	Ala	Ser	Arg	Leu	Gly	Trp	Ala
			115				120					125			
Leu	Gln	Asp	Ala	Thr	Leu	Val	Ser	Val	His	Gly	Arg	Pro	Leu	Asp	Leu
	130				135					140					
Val	Arg	Pro	His	Leu	His	Pro	Gly	Ala	Arg	Val	Leu	Thr	Leu	Thr	Ser
145				150					155						160
Asp	Gly	Ala	Gly	Pro	Arg	Asp	Leu	Ala	Glu	Leu	Leu	Val	Ser	Ser	Gly
				165					170					175	
Phe	Gly	Gln	Ser	Arg	Leu	Thr	Val	Leu	Glu	Ala	Leu	Gly	Gly	Ala	Gly
			180					185					190		
Glu	Arg	Val	Thr	Thr	Gln	Ile	Ala	Ala	Arg	Phe	Met	Leu	Gly	Leu	Val
	195						200					205			
His	Pro	Leu	Asn	Val	Cys	Ala	Ile	Glu	Val	Ala	Ala	Asp	Glu	Gly	Ala
	210					215					220				
Arg	Ile	Leu	Pro	Leu	Ala	Ala	Gly	Arg	Asp	Asp	Ala	Leu	Phe	Glu	His
225				230					235						240
Asp	Gly	Gln	Ile	Thr	Lys	Arg	Glu	Val	Arg	Ala	Leu	Thr	Leu	Ser	Ala
			245					250					255		
Leu	Ala	Pro	Arg	Lys	Gly	Glu	Leu	Leu	Trp	Asp	Ile	Gly	Gly	Gly	Ser
			260				265					270			
Gly	Ser	Ile	Gly	Ile	Glu	Trp	Met	Leu	Ala	Asp	Pro	Thr	Met	Gln	Ala
	275					280						285			
Ile	Thr	Ile	Glu	Val	Glu	Pro	Glu	Arg	Ala	Ala	Arg	Ile	Gly	Arg	Asn
	290					295					300				
Ala	Thr	Met	Phe	Gly	Val	Pro	Gly	Leu	Thr	Val	Val	Glu	Gly	Glu	Ala
305				310					315						320
Pro	Ala	Ala	Leu	Ala	Gly	Leu	Pro	Gln	Pro	Asp	Ala	Ile	Phe	Ile	Gly
			325					330					335		
Gly	Gly	Gly	Ser	Glu	Asp	Gly	Val	Met	Glu	Ala	Ala	Ile	Glu	Ala	Leu
			340					345					350		
Lys	Ser	Gly	Gly	Arg	Leu	Val	Ala	Asn	Ala	Val	Thr	Thr	Asp	Met	Glu
	355					360						365			
Ala	Val	Leu	Leu	Asp	His	His	Ala	Arg	Leu	Gly	Gly	Ser	Leu	Ile	Arg
	370				375						380				
Ile	Asp	Ile	Ala	Arg	Ala	Gly	Pro	Ile	Gly	Gly	Met	Thr	Gly	Trp	Lys
385				390					395						400
Pro	Ala	Met	Pro	Val	Thr	Gln	Trp	Ser	Trp	Thr	Lys	Gly			
			405						410						

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 762 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas denitrificans*
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:

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- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: cobM
- (B) LOCATION: 7172-7930 bp of SEQ ID NO: 2
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATGACGGTAC	ATTTTCATCGG	CGCCGGCCCCG	GGAGCCGCAG	ACCTGATCAC	GGTGCGTGGT	60
CGCGACCTGA	TCGGGGCGCTG	CCCGGTCTGC	CTTTACGCCG	GCTCGATCGT	CTCGCCGGAG	120
CTGCTGCGAT	ATTGCCCGCC	GGGCGCCCGC	ATTGTGCATA	CGGCGCCGAT	GTCCCTCGAC	180
GAGATCGAGG	CGGAGTATGT	GAAGGCCGAA	GCCGAAGGGC	TCGACGTGGC	GCGGCTTCAT	240
TCGGGGCGACC	TTTCGGTCTG	GAGTGCTGTG	GCCGAACAGA	TCCGCCGGCT	CGAGAAGCAT	300
GGCATCGCCT	ATACGATGAC	GCCGGGCGTT	CCTTCCTTTG	CGGCGGCGGC	TTCAGCGCTC	360
GGTCGCGAAT	TGACCATTCC	GGCCGTGGCC	CAGAGCCTGG	TGCTGACCCG	CGTTTCGGGC	420
CGCGCCTCGC	CGATGCCGAA	CTCAGAAACG	CTTTCGGCTT	TCGGCGCTAC	GGGATCGACG	480
CTGGCAATCC	ACCTTGCGAT	CCATGCGCTT	CAGCAGGTGG	TCGAGGAACT	GACGCCGCTC	540
TACGGTGCCG	ACTGCCCGGT	CGCCATCGTC	GTCAAGGCCT	CCTGGCCGGA	CGAACGCGTG	600
GTGCGCGGCA	CGCTCGGTGA	CATCGCCGCC	AAGGTGGCGG	AAGAGCCGAT	CGAGCGCACG	660
GCGCTGATCT	TCGTGCGTCC	GGGGCTCGAA	GCCTCCGATT	TCCGTGAAAG	CTCGCTCTAC	720
GATCCCGCCT	ATCAGCGGCG	CTTCAGAGGG	CGCGGCGAAT	AG		762

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBM
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met	Thr	Val	His	Phe	Ile	Gly	Ala	Gly	Pro	Gly	Ala	Ala	Asp	Leu	Ile
1				5				10						15	

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Thr Val Arg Gly Arg Asp Leu Ile Gly Arg Cys Pro Val Cys Leu Tyr
      20      25      30
Ala Gly Ser Ile Val Ser Pro Glu Leu Leu Arg Tyr Cys Pro Pro Gly
      35      40      45
Ala Arg Ile Val Asp Thr Ala Pro Met Ser Leu Asp Glu Ile Glu Ala
      50      55      60
Glu Tyr Val Lys Ala Glu Ala Glu Gly Leu Asp Val Ala Arg Leu His
      65      70      75      80
Ser Gly Asp Leu Ser Val Trp Ser Ala Val Ala Glu Gln Ile Arg Arg
      85      90      95
Leu Glu Lys His Gly Ile Ala Tyr Thr Met Thr Pro Gly Val Pro Ser
      100     105     110
Phe Ala Ala Ala Ser Ala Leu Gly Arg Glu Leu Thr Ile Pro Ala
      115     120     125
Val Ala Gln Ser Leu Val Leu Thr Arg Val Ser Gly Arg Ala Ser Pro
      130     135     140
Met Pro Asn Ser Glu Thr Leu Ser Ala Phe Gly Ala Thr Gly Ser Thr
      145     150     155     160
Leu Ala Ile His Leu Ala Ile His Ala Leu Gln Gln Val Val Glu Glu
      165     170     175
Leu Thr Pro Leu Tyr Gly Ala Asp Cys Pro Val Ala Ile Val Val Lys
      180     185     190
Ala Ser Trp Pro Asp Glu Arg Val Val Arg Gly Thr Leu Gly Asp Ile
      195     200     205
Ala Ala Lys Val Ala Glu Glu Pro Ile Glu Arg Thr Ala Leu Ile Phe
      210     215     220
Val Gly Pro Gly Leu Glu Ala Ser Asp Phe Arg Glu Ser Ser Leu Tyr
      225     230     235     240
Asp Pro Ala Tyr Gln Arg Arg Phe Arg Gly Arg Gly Glu
      245     250

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(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4748 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas denitrificans*
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:

- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION: Nucleotide Sequence of the 5' to 3' strand from the 4748 bp SalI-SalI-SalI-SalI-SalI-BglI fragment of *Pseudomonas denitrificans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GTGACGAGT	ATGGTCAGGT	TCAGGGTCTG	GTGACGCTGG	AGGACATTCT	GGAGGAGATC	60
GTGCGCGATA	TCGCCGATGA	GCACGACCTC	GACATTCAGG	GCGTGCGCCA	GGAAGCCGAT	120
GGCTCGATCG	TCGTCGATGG	CTCGGTGCCG	ATCCGCGATC	TCAACCGCGC	GCTCGACTGG	180
TCGCTGCCGG	ACGAGGAGGC	GACGACGGTG	GCCGGTCTGG	TCATCCACGA	GTCCAAGAGC	240
ATTCGGGAGG	AGCGCCAGGC	CTTCACCTTC	CACGGCAAAC	GCTTCATCGT	GATGAAGCGG	300
GTGAAGAACC	GCATTACCAA	GCTGCGCATC	CGTCCGGCGG	AAGAGGGTGC	TCCGCCGGCG	360
TGATGGCCGC	GATTGCCTCT	ACCAGCGGGT	CGGCTCGCCG	GGGGCTGCCG	GCTCGACGGC	420
GAGCGCATGC	AGGCCGGCGT	CGAGTTCTGG	CTTCAGGAGA	TCATTGATGG	CGCGGTGGCG	480
GGCGACACGG	CTCATGCCGG	CAAAGGCGCT	AGAAACGATA	CGCACCCGCA	TGTGGGACTC	540
GCCGGTACCA	TCGAAGCCCG	GCTGATGGCC	GGTATGCTGA	TGGCTCTCGT	TGATGACCTC	600
GAGCCGTTCA	GGGTGGAAGG	CCTCGATCAG	CTTCTTTTCG	ATGGTCTCGG	TGAGCGACAT	660
TCTTCCGTCC	CATTTTGCTG	TTTGCTTGGC	GCCCCCTCGC	AGTTAAGAAC	CCGTAATCG	720
CTGGCACGGC	GGCGCAAAT	GCCCGCACAA	AGCCAGCAAC	ATTCCGCTTT	GTCAATTCTT	780
GTTGTGACTC	CCGCCAAACC	CCATAATGAG	CGCCATGAGA	CTCGATTCAA	AATACTTCGA	840
TCGCATTCTGA	ACCCGGCGCA	AGGTCGAGCC	GCAGCAGAGC	CGGCGGCTCC	CGTCTGTCAG	900
TGGGACGGCT	GCGATCAGAA	GGGTGTGCAC	CGGGCGCCCG	TCGGTCGCAA	CGCCGAGGGG	960
CAGTACTTCA	TGTTCTGCTT	CGAGCAGGTG	AAGGAATACA	ACAAGGGCTA	CAACTTCTTC	1020
TCCGGCTCTCT	CCGACAGCGA	GGTCGCCCGC	TACCAGAAGG	AAGCGATCAC	CGGTATCCGG	1080
CCCACCTGGA	CCGTGCGCGT	CAACAAGAAC	GCCAAGAACG	GCCCGACCCA	GTCGCAGACG	1140
CGGTCTGGCT	CTGCCGGCGC	CCAGGCCCGC	ATGCGCGATC	CCTTCGGCTT	TGTCAGCGAG	1200
GCGCGGGCGC	GATCCGGTCG	TCCCGAGCCA	CGCCAGCGCA	AGCTGAAGAC	GCTCGAGGCG	1260
AAGGCCTTCG	AAACGCTTGG	TCTCGGAGCC	TCGGCGACCA	CTGCCGACAT	CAAGGCGGCC	1320
TACAAGGACC	TCGTCAAGAA	GCATCACCCC	GATGCCAATG	GCGGAGATAG	AGGATCGGAA	1380
GAGCGTTTTT	GCGCGTTTAT	TCAGGCCTAC	CAATTGTAA	AACAGGCTGG	TTTCTGCTAA	1440
CAACCCGGAT	TAATACAGAA	GCACTTTTGC	AGGCGAATGC	GCGGGTGCCG	TCCGGTGGCC	1500
GCTCTGGAGA	CATGATGAGC	AAGATTGACC	TCGACATTTT	CAACCTCCCC	GACACCACGA	1560
TTTCCGTCCG	GGAGGTTTTT	GGTATTGATA	CGGATTTGCG	CGTTCCTGCC	TATTCGAAGG	1620
GCGACGCCTA	TGTCCCGGAT	CTGGATCCGG	ACTACCTCTT	CGACCCGCAA	ACGACGCTCG	1680
CCATTCTCGC	AGGCTTCGCC	CACAACCGAC	GCGTGATGGT	GTCGGGCTAT	CACGGCACCG	1740
GCAAGTCCAC	CCATATCGAG	CAGGTCGCGC	CGCGCTCAA	CTGGCCGTGC	GTGCGCGTCA	1800
ACCTCGATAG	CCATGTCAGC	CGTATCGACC	TCGTGCGCAA	GGACGCGATC	GTCGTCAAGG	1860
ACGGCCTGCA	GGTCACCGAA	TTCAAGGACG	GCATCCTGCC	CTGGGCCTAC	CAGCACAATG	1920
TCGCGCTCGT	CTTCGACGAA	TACGATGCCG	GCCGCCCGGA	CGTCATGTTC	GTCATCCAGC	1980
GCGTGCTGGA	ATCCTCCGGC	CGCCTGACGC	TGCTCGACCA	GAGCCGTGTC	ATCCGTCCGC	2040
ACCCGGCCTT	CCGCTGTITT	GCGACCGCCA	ACACCGTCGG	CCTCGGCGAC	ACGACCGGCC	2100
TCTATCACGG	CACGCGCAG	ATCAACCAGG	CGCAGATGGA	CCGCTGGTCG	ATCGTCACCA	2160
CGCTGAACCTA	CCTGCCGCAC	GACAAGGAAG	TCGACATCGT	CGCCGCCAAG	GTCAAGGGCT	2220
TCACCGCCGA	CAAGGGCCGC	GAGACCGTCT	CCAAGATGGT	ACGTGTCGCC	GACCTCACGC	2280
GCGCAGCCTT	CATCAATGGC	GATCTCTCGA	CTGTCATGAG	CCCGCGTACG	GTCATCACCT	2340
GGGCCGAGAA	CGCCACATC	TTCCGGCGACA	TCGCTTTTCG	CTTCCGCGTG	ACCTTCCTCA	2400
ACAAGTCGGA	CGAGCTGGAG	CGGGCGCTGG	TCGCCGAGCA	CTACCAGCGC	GCCTTCGGCA	2460
TCGAGCTGAA	GGAATGCGCT	GCCAACATCG	TGCTCGAAGC	CACCGCCTGA	TCCCACGGCC	2520
TGCCGTCCCC	TTTGGGAGGG	CGGGTCATGA	CGCTGTGGCA	AACCGGATGA	CGCCCCACTG	2580
GGGCGCCGTC	GCCTCTGGCT	GAAGAAGGAA	CTGTCGTGAG	CTCGAATTCT	AAGGCAAAGC	2640
CAACCACGCG	CGAGAATGCT	GCGGAACCGT	TCAAGCGGGC	GCTTTCGGGC	TGCATCCGAT	2700
CGATCGCGGG	CGATGCCGAG	GTGGAAGTCG	CCTTCGCCAA	CGAGCGGCCG	GGCATGACCG	2760
GCGAACGCAT	CCGTCTGCCG	GAACTTTCCA	AGCGCCCGAC	CCTGCAGGAA	CTTGCCGTGA	2820
CCCGCGGGCT	CGGTGACAGC	ATGGCGCTGC	GCAAGGCCTG	TACGCATGCG	CGGATCCAGC	2880
GCACCATGTC	GCCGCAAGGG	GCGGACGCCC	GCGCGATCTT	CGATGCGGTG	GAGCAGGCTC	2940
GTGTCGAGGC	GATCGGGTCG	TTGCGCATGG	CGGGTGTGCG	CAAGAACCTC	AACGTTCATGC	3000
TCGAAGAGAA	ATACGCCAAG	GCGAATTTTC	CAACGATCGA	GCGCCAGGCG	GACGCGCCGC	3060
TCGGCGGAGG	CGTAGCGCTG	CTGGTGCGCG	AGAAGCTGAC	GGGCCAGAAG	CCGCCGGCGT	3120
CTGCCGGCAA	GGTGCTCGAC	CTTGCCGCGG	AGTTTCATCGA	GGGCAAGGCT	GCCGGCGACA	3180
TTGAGCACCT	TCGCTCGACG	ATCAACAACC	AGCAGGCCTT	TGCCCGGGTC	GTTTCGCGACA	3240
TGCTGACCTC	GATGGAAGTC	GCCGAGAAAT	ACGGTGACGA	CGACAACGAG	CCGGACGAGC	3300
AGGAAAGCGA	GACCGACGAA	GACCAGCCGC	GCAGCCAGGA	GCAGGACGAG	AACGCCAGCG	3360
ACGAGGAAGC	CGGCGACGAT	GCCGCACCCG	CCGACGAGAA	CCAGGCTGCC	GAAGAGCAGA	3420
TGGAAGAAGG	CGAGATGGAC	GGCGCGGAGA	TCTCCGACGA	CGATCTCCAG	GACGAAGGCG	3480
ACGAGGACAG	GCGAACGCCC	GGCGAGGTCA	AGCGTCCGAA	CCAGCCCTTC	GCCGACTTCA	3540
ACGAGAAGGT	CGACTACGCC	GTCTTCACCC	GCGAGTTCGA	CGAGACGATT	GCCTCGGAAG	3600

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AGCTTTGCGA	CGAGGCCGAG	CTCGACCGGC	TGCGCGCCTT	CCTCGACAAG	CAGCTTGCCC	3660
ATCTTCAAGG	CGCGGTGCGC	CGCCTTGCCA	ACCGGCTGCA	GCGCCGCCTG	ATGGCGCAGC	3720
AGAACCGCTC	CTGGGAGTTC	GATCTCGAAG	AGGGGTATCT	CGATTGCGCG	CGGCTTCAGC	3780
GCATCATCAT	CGATCCGATG	CAGCCGCTTT	CCTTCAAGCG	CGAAAAGGAC	ACCAACTTCC	3840
GCGATACCGT	CGTGACGCTG	CTGATCGACA	ATTCCGGCTC	GATGCGCGGC	CGTCCGATCA	3900
CGGTTGCCGC	CACCTGCGCC	GATATCCTGG	CGCGCACGCT	CGAGCGCTGC	GGCGTCAAGG	3960
TCGAGATCCT	CGGTTTTACC	ACCAAGGCGT	GGAAGGGTGG	GCAGTCACGC	GAGAAGTGGC	4020
TGGCCGGCGG	CAAGCCACAG	GCCCCGGGTC	GCCTCAACGA	CCTGCGACAC	ATCGTCTACA	4080
AGTCTGCCGA	CGTCCGTGG	CGCCGGGCAC	GACGCAATCT	CGGCCTGATG	ATGCGGGAAG	4140
GCCTGCTCAA	GGAAAACATC	GACGGCGAGG	CGTTGATTTG	GGCGCATGAG	CGGCTGATGG	4200
CGCGGCGCGA	ACAGCGGCGC	ATCCTGATGA	TGATTTGCGA	CGGCGCGCCG	GTCGACGACT	4260
CGACGCTGTC	GGTCAATCCA	GGAAACTATC	TGGAGCGTCA	CCTGCGCGCG	GTCATCGAGC	4320
AGATCGAAAC	GCGCTCGCCG	GTGGAAGTGC	TGGCGATCGG	TATCGGCCAC	GACGTGACGC	4380
GCTACTATCG	CCGTGCCGTC	ACCATCGTCG	ATGCCGATGA	GCTTGCCGGC	GCGATGACCG	4440
AACAGCTGGC	CGCACTCTTC	GAGGACGAAA	GCCAGCGCCG	CGGTTCTTCG	CGTCTTCGCC	4500
GCGCCGGGTG	ATGCTTCCCC	CTTGGGGGCG	GTGGAACATC	GCCTCCGAGC	TGCCAATCGG	4560
CACCTGCACG	CATCGCTGGC	GGCCGAAGTC	AATTTACGGA	CATAGTTTTA	CAGTCTACCA	4620
AGCTACCATG	CGTGGCGGGC	TCACTTTGAG	CGCACGCCGC	GTCATTCCCG	ATGCCCCCTG	4680
AAGGTACTTC	TCTTGATGCT	TGGCCGCGGT	CTCCTAGCCC	TTTTCTCCT	GGCTTCGGCC	4740
TGCCCCGC						4748

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3855 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Nucleotide sequence of the 5' to 3'

strand from the 3855 bp SstI-SstI-BamHI fragment of *Pseudomonas denitrificans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

GAGCTCATAG	AGCAGTTCCT	CGATCGACTT	CAGCAGTCGC	ATGAAATCCA	TGCCGTGCTC	60
CCCTTGCTTC	TATGCGTGGC	ACGACCGCGC	GCCGGGGCCG	ATGCCGGTCA	GTCGCGCAGA	120
CGCAGCTCGT	CGGTACGCAT	CTGCAGCATC	TCCAGCGTCG	ACAGGAAGCT	CATGCCGAGC	180
AGGCTCTGAT	CGAGCTTGCC	CTTGGCTGCG	ACCGTTGCGC	CGATGTTGCG	GCGGGTGATC	240
GGGCCGATCG	AGATCTCCTG	AAGCATCACG	GGGGCTGCCT	GGGCCCGGCC	ATTGGCTGTC	300
ATGACCGTGA	CGATAAAGTT	GAGGTTGGCC	GGGTCGAGGC	CGATCTTTTC	CGCATCTTCA	360
TAGGTGAGCG	CGATGTTGCT	GCGCCGGGTA	TCGACCAGCA	TGCTGATGTC	CTTGCCGTCG	420
ACCGTCGCAG	TGGTCTCGAA	ATGACCGTTC	AGCATCTTCT	GCAGACCAC	TTCCTGCTGT	480

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CCCTCGCTGT	CAGTGATGAT	GGTGGCGCGG	CCGGGGATGA	GGCCGGCGAG	CAGGCGGTTA	540
CCGAAGCCCT	CCAACCTCGAA	GCGGTAGACA	TAGGCCGAGA	CCAGCGCCAG	AACGACGAAG	600
AGCCAGATGG	CGATCTGACG	CAGGCCTTCG	CCGAAGCGGT	GGCGGCTCTG	CAGGATGCCG	660
GCGCCGATCA	GCGTGGCGAT	GGCGCCGAGC	GAGACCAGTT	GCCCGAACTG	GTCATTGGCA	720
AGCCCCATGG	TGCGGCCGGT	GTCGTGGTTG	ATGATCAGCA	GGATGAGGCC	GATGGCCAGG	780
ATCGAGAGCA	GGATGGCAAG	ACGGGTCATG	CTTCGCCGCG	TTCCCTCGCC	ATGCGCGTGC	840
GTCGGGTTTT	GCGCCGCGGC	TTGCGTTCGA	CGGTCTCAAG	CCGTGCAGGC	AACGCGCTCA	900
TGATCGCGCG	GCGTTCGGCA	TCGGTATAGA	GCGTCCAGCG	TCCGACTTCG	TCGCGGGTAC	960
GGCCGCAGCC	GAAACAGTAG	CCGGTCTTGT	CATCGATCGA	ACAGACGAGA	ATGCAGGGAG	1020
ATTCCATGGG	CGTGCTCAGT	TTTCCCTTGA	TATATCGATG	TTTCAAACCG	TCAGCGCAAG	1080
GGCACCAGAGC	ACGGCGATTT	CGGTCACTTG	CTGCGTCGCC	CCGATCGTGT	CGCCCGTTTG	1140
TCCGCCGATC	TTGCGCATCG	CCAGCCGAGC	GAAGCCCTTG	ACCGTGGCAA	GGAATGCGAC	1200
GAGCGCCGCG	ATGACGCCGA	GCGCCGGGAC	CTGCGCGAGA	TAGAAGAGCA	GCATTGCGAC	1260
AAGAAGTCCG	AAGGCAAGCG	CGAAGCGCGT	GGCCGCCGGT	TCCGGCTCGC	CAGCCGAGGC	1320
CGCGACGCCG	CTGCTGCGCG	CCGGCGGAAG	CGACGACCAG	TGCCAGACCA	TGGCGGCGCG	1380
GCTGAGGCAC	GCTGCGCCAA	GGATCGCCAT	GGCGGCGCCC	AGCGGCGAAA	AGAGCGGCAG	1440
GATCGAGGCG	AACGCCGAGA	CGCGCAGGCC	GAAGGAGAGG	ATGAGGGCGA	CGGCCGCATA	1500
GGTGCCGATG	CGGCTGTCCT	TCATGATCGC	AAGCGCCGCT	TCGCGGTTCG	GACCGCCGCC	1560
AAAGCCATCG	GCCGTGTTCG	CAAGCCCCTG	TTCTGTGAGT	GCGCCGGTGA	CAAGCGCCTG	1620
GATGGCGACG	ACGACAAAGG	CGGCAAAAGG	CGAGCTCACC	TGCAGCGCCA	TGAGGGCCAT	1680
GGCGACGGCC	GCCGATGGCA	GTGCGATCGC	CAGGCCGGCG	AACGGGAAGG	CGCGCACGGC	1740
ACGGCTCAAG	CGCCCGTCAT	AACCTTCGAA	ATGACGCGCA	GGCATCGGGA	TGCGGCTGAG	1800
AAAGCCGATC	GACCGCGCCA	CATCGTCACA	GAAATCGCCA	ACGAAGCCCA	TGGCTCCTCC	1860
AAGGTTGCGG	CCATTGACCC	GGCCGCTGCC	AAACTCGCCG	ACTGCGGCGA	GTCTCGCAAG	1920
CCGGGCGGGG	GCACCCGCGA	GGGCGCGCGA	CACTTTTCCC	AGACCTTTCA	TAGGCCGTCT	1980
GCGACCGCTC	ACGGATCGAG	ACGGCGACGC	GCAATTGGCG	AAATGTCGTT	GCCCGAATTT	2040
TCGGCGCCCT	CTATGAGGGG	CGTAGATAGA	GCTTCACGAT	GATGCAAGGA	TTCTCCCAT	2100
GAGTGCCAGC	GGCCTGCCGT	TTGATGATTT	TCGCGAATTG	TTGCGCAACC	TGCCGGGCCC	2160
GGATGCGGCA	GCCCTCGTTG	CCGCGCGGGA	GCGGGACGCC	CAGCTGACGA	AGCCGCCGGG	2220
CGCGCTCGGC	CGCCTCGAGG	AAATCGCCTT	CTGGCTCGCC	GCCTGGACGG	GCAAGGCGCC	2280
GGTGGTCAAC	CGCCCGCTGG	TGGCGATCTT	TGCCGGCAAC	CACGGCGTCA	CCCGCCAGGG	2340
GGTGACCCCG	TTCCCGTATG	CCGTCAACCG	ACAGATGGTC	GAGAATTTTG	CCGCGGCTGG	2400
CGCTGCGATC	AACCAGATCT	GCGTCAGCCA	CGACCTCGGG	CTGAAGGTCT	TCGACCTCGC	2460
ACTCGAATAC	CCGACCGGTG	ATATACCCGA	GGAAGCCGCG	CTGTCCGAGC	GCGATTGCGC	2520
CGCGACCATG	GCCTTTGGCA	TGGAGGCGAT	TGCCGGCGGC	ACGGATCTTC	TGTGCATCGG	2580
CGAAATGGGC	ATCGGCAACA	CCACGATCGC	GGCCGCGATC	AATCTCGGCC	TTTATGGTGG	2640
CACGGCCGAA	GAATGGGTCT	GTCCGGGTAC	CGGCTCCGAG	GGCGAGGTGC	TGAAGCGCAA	2700
GATCGCCGCG	GTCGAAAAGG	CCGTGGCGCT	GCATCGCGAT	CACCTGTCCG	ATCCGCTCGA	2760
ACTGATGCGT	CGCCTCGGCG	GTCGTGAGAT	CGCGGCCATG	GCTGGCGCCA	TCCTGGCCGC	2820
CCGCGTCCAG	AAGGTACCTG	TCATCATCGA	CGGCTACGTG	GCGACCGCTG	CGGCTTCGAT	2880
CCTGAAGGCG	GCCAACCCGT	CGGCCCTCGA	CCATTGCCTG	ATCGGCCATG	TTTCGGGCGA	2940
ACCGGGGCAT	CTGCGCGCGA	TCGAGAAGCT	CGGCAAGACG	CCGCTGCTGG	CACTCGGCAT	3000
GCGGCTTGGC	GAAGGACCGG	GCGCGGCCCT	TGCCGCGCGT	ATCGTCAAGG	CGGCGGCCGC	3060
TTGCCACAGC	GGCATGCGCA	CCTTTGCCCA	CCGCGCGCTC	AGCAACAAGG	AATAGTGAAG	3120
TTCCGGCCGG	GCTTTGCAGG	AAGGCCGGCC	GGTTTCTGTC	CAAGGCCTGT	CACGGGCGCG	3180
AAGCTGTCTG	GTGCCGGGCC	TTGATGGATG	CGTCTTCTC	GCCTATCCAA	AGCGCAAATG	3240
CGCGCCCTAG	CTATAGTCTT	GGGTGCCTGC	AACCGAGACC	GCCTTGCAAT	CGCCTCAATC	3300
ACGATGTCGA	AGCAAGCACA	GTTTCAAGCC	CTGTCGAGAC	GAAATGGACG	CCAAGAACAC	3360
CACGCACCGC	ATTGGACAGA	CGGGTCCTGT	CGAGAAGCAG	ACCGGCATTG	GGCATCTCTT	3420
TGCGCTGCG	AGCTATTTCG	TCGGCGGCGC	CAAGCGGCTG	ATCGGCGAGG	CTGCCCTTCG	3480
CCACGAGCTG	ATCGCCTTTG	CCGCCGCGAT	GATCGCTTTC	ATCATCGTCG	GCGCAACCTT	3540
CTTCCAATAT	GTGGCGATGG	CGATCCTGTT	CCTGCTGATG	ATGGCCTTCG	AGGCGATCAA	3600
CACGGCAATC	GAGGAAATTG	TCGATCGCGT	TTCTCCCGAA	ATCTCGGAAA	TGGGTAAGAA	3660
CGCCAAGGAT	CTCGGCTCCT	TCGCCTGCCT	CTGCCTGATT	GTCGCCAACG	GTGTCTATGC	3720
CGCCTATGTC	GTGATCTTCG	ACGGCTTCAT	GAAGTGACCG	GCTAGCGGGC	CGGCGCCTTC	3780
ACCCGATAAA	GCACATGCGG	ACGCAGCGGG	TTGCCCCCGG	GTACCGTGAC	GTCGTGAAAA	3840
TCATCAGCCG	GATCC					3855

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 999 base pairs
 (B) TYPE: Nucleic Acid

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- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: Pseudomonas denitrificans
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: cobs
- (B) LOCATION: 1512-2510 bp of SEQ ID NO: 29
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATGATGAGCA	AGATTGACCT	CGACATTTCC	AACCTCCCCG	ACACCACGAT	TTCCGTCCGG	60
GAGGTTTTTCG	GTATTGATAC	GGATTTGCGC	GTTCTGCTGCT	ATTCGAAGGG	CGACGCCTAT	120
GTCCCGGATC	TGGATCCGGA	CTACCTCTTC	GACCGCGAAA	CGACGCTCGC	CATTCTCGCA	180
GGCTTCGCCC	ACAACCGACG	CGTGATGGTG	TCGGGCTATC	ACGGCACCGG	CAAGTCCACC	240
CATATCGAGC	AGGTCGCCGC	GCGCCTCAAC	TGGCCGTGCG	TGCGCGTCAA	CCTCGATAGC	300
CATGTCAGCC	GTATCGACCT	CGTCGGCAAG	GACGCGATCG	TCGTCAAGGA	CGGCCTGCAG	360
GTCACCGAAT	TCAAGGACGG	CATCCTGCCC	TGGGCCTACC	AGCACAATGT	CGCGCTCGTC	420
TTCGACGAAT	ACGATGCCGG	CCGCCCCGGAC	GTCATGTTTCG	TCATCCAGCG	CGTGCTGGAA	480
TCCTCCGGCC	GCCTGACGCT	GCTCGACCAG	AGCCGTGTCA	TCCGTCCGCA	CCCGGCCTTC	540
CGCCTGTTTG	CGACCGCCAA	CACCGTCGGC	CTCGGCGACA	CGACCGGCCT	CTATCACGGC	600
ACGCAGCAGA	TCAACCAGGC	GCAGATGGAC	CGCTGGTCTGA	TCGTCAACCAC	GCTGAACTAC	660
CTGCCGCACG	ACAAGGAAGT	CGACATCGTC	GCCGCCAAGG	TCAAGGGCTT	CACCGCCGAC	720
AAGGGCCGCG	AGACCGTCTC	CAAGATGGTA	CGTGTGCGCG	ACCTCACGCG	CGCAGCCTTC	780
ATCAATGGCG	ATCTCTCGAC	TGTCATGAGC	CCGCGTACGG	TCATCACCTG	GGCCGAGAAC	840
GCCCACATCT	TCGGCGACAT	CGCTTTTCGCC	TTCCGCGTGA	CCTTCCTCAA	CAAGTGCAGC	900
GAGCTGGAGC	GGGCGCTGGT	CGCCGAGCAC	TACCGAGCGC	CCTTCGGCAT	CGAGCTGAAG	960
GAATGCGCTG	CCAACATCGT	GCTCGAAGCC	ACCGCCTGA			999

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: Amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: Pseudomonas denitrificans
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:

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(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(ix) FEATURE:

(A) NAME/KEY: COBS
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Translation product of SEQ ID NO:31

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met	Met	Ser	Lys	Ile	Asp	Leu	Asp	Ile	Ser	Asn	Leu	Pro	Asp	Thr	Thr
1				5				10						15	
Ile	Ser	Val	Arg	Glu	Val	Phe	Gly	Ile	Asp	Thr	Asp	Leu	Arg	Val	Pro
		20					25					30			
Ala	Tyr	Ser	Lys	Gly	Asp	Ala	Tyr	Val	Pro	Asp	Leu	Asp	Pro	Asp	Tyr
		35				40					45				
Leu	Phe	Asp	Arg	Glu	Thr	Thr	Leu	Ala	Ile	Leu	Ala	Gly	Phe	Ala	His
	50				55					60					
Asn	Arg	Arg	Val	Met	Val	Ser	Gly	Tyr	His	Gly	Thr	Gly	Lys	Ser	Thr
65				70				75						80	
His	Ile	Glu	Gln	Val	Ala	Ala	Arg	Leu	Asn	Trp	Pro	Cys	Val	Arg	Val
			85					90					95		
Asn	Leu	Asp	Ser	His	Val	Ser	Arg	Ile	Asp	Leu	Val	Gly	Lys	Asp	Ala
		100					105					110			
Ile	Val	Val	Lys	Asp	Gly	Leu	Gln	Val	Thr	Glu	Phe	Lys	Asp	Gly	Ile
	115				120					125					
Leu	Pro	Trp	Ala	Tyr	Gln	His	Asn	Val	Ala	Leu	Val	Phe	Asp	Glu	Tyr
	130				135					140					
Asp	Ala	Gly	Arg	Pro	Asp	Val	Met	Phe	Val	Ile	Gln	Arg	Val	Leu	Glu
145				150				155						160	
Ser	Ser	Gly	Arg	Leu	Thr	Leu	Leu	Asp	Gln	Ser	Arg	Val	Ile	Arg	Pro
			165					170					175		
His	Pro	Ala	Phe	Arg	Leu	Phe	Ala	Thr	Ala	Asn	Thr	Val	Gly	Leu	Gly
		180					185						190		
Asp	Thr	Thr	Gly	Leu	Tyr	His	Gly	Thr	Gln	Gln	Ile	Asn	Gln	Ala	Gln
	195					200					205				
Met	Asp	Arg	Trp	Ser	Ile	Val	Thr	Thr	Leu	Asn	Tyr	Leu	Pro	His	Asp
	210				215					220					
Lys	Glu	Val	Asp	Ile	Val	Ala	Ala	Lys	Val	Lys	Gly	Phe	Thr	Ala	Asp
225				230				235						240	
Lys	Gly	Arg	Glu	Thr	Val	Ser	Lys	Met	Val	Arg	Val	Ala	Asp	Leu	Thr
			245					250					255		
Arg	Ala	Ala	Phe	Ile	Asn	Gly	Asp	Leu	Ser	Thr	Val	Met	Ser	Pro	Arg
		260					265					270			
Thr	Val	Ile	Thr	Trp	Ala	Glu	Asn	Ala	His	Ile	Phe	Gly	Asp	Ile	Ala
	275					280						285			
Phe	Ala	Phe	Arg	Val	Thr	Phe	Leu	Asn	Lys	Cys	Asp	Glu	Leu	Glu	Arg
	290				295					300					
Ala	Leu	Val	Ala	Glu	His	Tyr	Gln	Arg	Ala	Phe	Gly	Ile	Glu	Leu	Lys
305				310				315						320	
Glu	Cys	Ala	Ala	Asn	Ile	Val	Leu	Glu	Ala	Thr	Ala				
			325					330							

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1896 base pairs
(B) TYPE: Nucleic acid

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- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: cobT
(B) LOCATION: 2616-4511 bp of SEQ ID NO: 29
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GTGAGCTCGA	ATTCTGAAGGC	AAAGCCAACC	ACGCGCGAGA	ATGCTGCGGA	ACCGTTCAAG	60
CGGGCGCTTT	CCGGCTGCAT	CCGATCGATC	GCGGGCGATG	CCGAGGTGGA	AGTCGCCTTC	120
GCCAACGAGC	GGCCGGGCAT	GACCGGCGAA	CGCATCCGTC	TGCCGGAAC	TTCCAAGCGC	180
CCGACCCTGC	AGGAACCTGC	CGTGACCCGC	GGGCTCGGTG	ACAGCATGGC	GCTGCGCAAG	240
GCCTGTACGC	ATGCGCGGAT	CCAGCGCACC	ATGTCGCCGC	AAGGGGCGGA	CGCCCGCGCG	300
ATCTTCGATG	CGGTGGAGCA	GGCTCGTGTC	GAGGCGATCG	GGTCGTTGCG	CATGGCGGGT	360
GTCGCAAGA	ACCTCAACGT	CATGCTCGAA	GAGAAATACG	CCAAGGCGAA	TTTCGCAACG	420
ATCGAGCGCC	AGGCGGACGC	GCCGCTCGGC	GAGGCCGTAG	CGCTGCTGGT	GCGCGAGAAG	480
CTGACGGGCC	AGAAGCCGCG	GGCGTCTGCC	GGCAAGGTGC	TCGACCTCTG	GCGCGAGTTC	540
ATCGAGGGCA	AGGCTGCCGC	CGACATTGAG	CACCTGTCTG	CGACGATCAA	CAACCAGCAG	600
GCCTTTGCC	GGGTCGTTTC	CGACATGCTG	ACCTCGATGG	AAGTCGCCGA	GAAATACGGT	660
GACGACGACA	ACGAGCCGGA	CGAGCAGGAA	AGCGAGACCG	ACGAAGACCA	GCCGCGCAGC	720
CAGGAGCAGG	ACGAGAACGC	CAGCGACGAG	GAAGCCGGCG	ACGATGCCGC	ACCCGCCGAC	780
GAGAACCAGG	CTGCCGAAGA	GCAGATGGAA	GAAGGCGAGA	TGGACGGCGC	GGAGATCTCC	840
GACGACGATC	TCCAGGACCA	AGGCGACGAG	GACAGCGAAA	CGCCCGGCGA	GGTCAAGCGT	900
CCGAACCAGC	CCTTCGCCGA	CTTCAACGAG	AAGGTCGACT	ACGCCGTCTT	CACCCGCGAG	960
TTTCGACGAG	CGATTGCCCT	GGAAGAGCTT	TGCGACGAGG	CCGAGCTCGA	CCGGCTGCGC	1020
GCCTTCCTCG	ACAAGCAGCT	TGCCCATCTT	CAAGGCGCGG	TCGGCCGCCT	TGCCAACCAG	1080
CTGACGCGCC	GCCTGATGGC	GCAGCAGAAC	CGCTCCTGGG	AGTTCGATCT	CGAAGAGGGG	1140
TATCTCGATT	CGGCGCGGCT	TCAGCGCATC	ATCATCGATC	CGATGCAGCC	GCTTTCCTTC	1200
AAGCGCGAAA	AGGACACCAA	CTTCCGCGAT	ACCGTCGTGA	CGCTGCTGAT	CGACAATTCC	1260
GGCTCGATGC	GCGGCCGTCC	GATCACGGTT	GCCGCCACCT	GCGCCGATAT	CCTGGCGCGC	1320
ACGCTCGAGC	GCTGCGGCGT	CAAGGTCGAG	ATCCTCGGTT	TTACCACCAA	GGCGTGGAAG	1380
GGTGGGCAGT	CACGCGAGAA	GTGGCTGGCC	GGCGGCAAGC	CACAGGCCCC	GGGTCGCCTC	1440
AACGACCTGC	GACACATCGT	CTACAAGTCT	GCCGACGCTC	CGTGGCGCCG	GGCACGACGC	1500
AATCTCGGCC	TGATGATGCG	GGAAGGCCTG	CTCAAGGAAA	ACATCGACGG	CGAGGCGTTG	1560
ATTTGGGCGC	ATGAGCGGCT	GATGGCGCGG	CGCGAACAGC	GGCGCATCCT	GATGATGATT	1620
TCGGACGGCG	CGCCGGTCGA	CGACTCGAGC	CTGTCCGTCA	ATCCAGGAAA	CTATCTGGAG	1680
CGTCACCTGC	GCGCGGTCAT	CGAGCAGATC	GAAACGCGCT	CGCCGGTGGA	ACTGCTGGCG	1740
ATCGGTATCG	GCCACGACGT	GACGCGCTAC	TATCGCCGTG	CCGTCACCAT	CGTCGATGCC	1800
GATGAGCTTG	CCGGCGCGAT	GACCGAACAG	CTGGCCGCAC	TCTTCGAGGA	CGAAAGCCAG	1860
CGCCGCGGTT	CTTCGCGTCT	TCGCCGCGCC	GGGTGA			1896

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 631 amino acids
- (B) TYPE: Amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: Pseudomonas denitrificans
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBT
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

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Val Ser Ser Asn Ser Lys Ala Lys Pro Thr Thr Arg Glu Asn Ala Ala
1      5      10      15
Glu Pro Phe Lys Arg Ala Leu Ser Gly Cys Ile Arg Ser Ile Ala Gly
20      25      30
Asp Ala Glu Val Glu Val Ala Phe Ala Asn Glu Arg Pro Gly Met Thr
35      40      45
Gly Glu Arg Ile Arg Leu Pro Glu Leu Ser Lys Arg Pro Thr Leu Gln
50      55      60
Glu Leu Ala Val Thr Arg Gly Leu Gly Asp Ser Met Ala Leu Arg Lys
65      70      75      80
Ala Cys Thr His Ala Arg Ile Gln Arg Thr Met Ser Pro Gln Gly Ala
85      90      95
Asp Ala Arg Ala Ile Phe Asp Ala Val Glu Gln Ala Arg Val Glu Ala
100     105     110
Ile Gly Ser Leu Arg Met Ala Gly Val Ala Lys Asn Leu Asn Val Met
115     120     125
Leu Glu Glu Lys Tyr Ala Lys Ala Asn Phe Ala Thr Ile Glu Arg Gln
130     135     140
Ala Asp Ala Pro Leu Gly Glu Ala Val Ala Leu Val Arg Glu Lys
145     150     155     160
Leu Thr Gly Gln Lys Pro Pro Ala Ser Ala Gly Lys Val Leu Asp Leu
165     170     175
Trp Arg Glu Phe Ile Glu Gly Lys Ala Ala Gly Asp Ile Glu His Leu
180     185     190
Ser Ser Thr Ile Asn Asn Gln Gln Ala Phe Ala Arg Val Val Arg Asp
195     200     205
Met Leu Thr Ser Met Glu Val Ala Glu Lys Tyr Gly Asp Asp Asp Asn
210     215     220
Glu Pro Asp Glu Gln Glu Ser Glu Thr Asp Glu Asp Gln Pro Arg Ser
225     230     235     240
Gln Glu Gln Asp Glu Asn Ala Ser Asp Glu Glu Ala Gly Asp Asp Ala
245     250     255
Ala Pro Ala Asp Glu Asn Gln Ala Ala Glu Glu Gln Met Glu Glu Gly

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Glu	Met	Asp	260	Gly	Ala	Glu	Ile	Ser	265	Asp	Asp	Asp	Leu	Gln	270	Asp	Glu	Gly
Asp	Glu	Asp	275	Ser	Glu	Thr	Pro	Gly	280	Glu	Val	Lys	Arg	Pro	285	Asn	Gln	Pro
Phe	Ala	Asp	290	Phe	Asn	Glu	Lys	Val	295	Asp	Tyr	Ala	Val	Phe	300	Thr	Arg	Glu
Phe	Asp	Glu	305	Thr	Ile	Ala	Ser	Glu	310	Glu	Leu	Cys	Asp	Glu	315	Ala	Glu	Leu
Asp	Arg	Leu	320	Arg	Ala	Phe	Leu	Asp	325	Lys	Gln	Leu	Ala	His	330	Leu	Gln	Gly
Ala	Val	Gly	335	Arg	Leu	Ala	Asn	Arg	340	Leu	Gln	Arg	Arg	Leu	345	Met	Ala	Gln
Gln	Asn	Arg	350	Ser	Trp	Glu	Phe	Asp	355	Leu	Glu	Glu	Gly	Tyr	360	Leu	Asp	Ser
Ala	Arg	Leu	365	Gln	Arg	Ile	Ile	Ile	370	Asp	Pro	Met	Gln	Pro	375	Leu	Ser	Phe
Lys	Arg	Glu	380	Lys	Asp	Thr	Asn	Phe	385	Arg	Asp	Thr	Val	Val	390	Thr	Leu	Leu
Ile	Asp	Asn	395	Ser	Gly	Ser	Met	Arg	400	Gly	Arg	Pro	Ile	Thr	405	Val	Ala	Ala
Thr	Cys	Ala	410	Asp	Ile	Leu	Ala	Arg	415	Thr	Leu	Glu	Arg	Cys	420	Gly	Val	Lys
Val	Glu	Ile	425	Leu	Gly	Phe	Thr	Thr	430	Lys	Ala	Trp	Lys	Gly	435	Gly	Gln	Ser
Arg	Glu	Lys	440	Trp	Leu	Ala	Gly	Gly	445	Lys	Pro	Gln	Ala	Pro	450	Gly	Arg	Leu
Asn	Asp	Leu	455	Arg	His	Ile	Val	Tyr	460	Lys	Ser	Ala	Asp	Ala	465	Pro	Trp	Arg
Arg	Ala	Arg	470	Arg	Asn	Leu	Gly	Leu	475	Met	Met	Arg	Glu	Gly	480	Leu	Leu	Lys
Glu	Asn	Ile	485	Asp	Gly	Glu	Ala	Leu	490	Ile	Trp	Ala	His	Glu	495	Arg	Leu	Met
Ala	Arg	Arg	500	Glu	Gln	Arg	Arg	Ile	505	Leu	Met	Met	Ile	Ser	510	Asp	Gly	Ala
Pro	Val	Asp	515	Asp	Ser	Thr	Leu	Ser	520	Val	Asn	Pro	Gly	Asn	525	Tyr	Leu	Glu
Arg	His	Leu	530	Arg	Ala	Val	Ile	Glu	535	Gln	Ile	Glu	Thr	Arg	540	Ser	Pro	Val
Glu	Leu	Leu	545	Ala	Ile	Gly	Ile	Gly	550	His	Asp	Val	Thr	Arg	555	Tyr	Tyr	Arg
Arg	Ala	Val	560	Thr	Ile	Val	Asp	Ala	565	Asp	Glu	Leu	Ala	Gly	570	Ala	Met	Thr
Glu	Gln	Leu	575	Ala	Ala	Leu	Phe	Glu	580	Asp	Glu	Ser	Gln	Arg	585	Arg	Gly	Ser
Ser	Arg	Leu	590	Arg	Arg	Ala	Gly		595						600			
			605						610						615			
			620						625						630			

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas denitrificans*

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- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: cobX
- (B) LOCATION: 4089-4370 bp of SEQ ID NO:29
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATGTCGCTCA	CCGAGACCAT	CGAAAAGAAG	CTGATCGAGG	CCTTCCACCC	TGAACGGCTC	60
GAGGTCATCA	ACGAGAGCCA	TCAGCATACC	GGCCATCAGC	CGGGCTTCGA	TGGTACCGGC	120
GAGTCCCACA	TGCGGGTGCG	TATCGTTTCT	AGCGCCTTTG	CCGGCATGAG	CCGTGTCGCC	180
CGCCACCGCG	CCATCAATGA	TCTCCTGAAG	CCAGAACTCG	ACGCCGGCCT	GCATGCGCTC	240
GCCGTCGAGC	CGGCAGCCCC	CGGCGAGCCG	ACCCGCTGGT	AG		282

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: Amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: Pseudomonas denitrificans
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBX
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Met	Ser	Leu	Thr	Glu	Thr	Ile	Glu	Lys	Lys	Leu	Ile	Glu	Ala	Phe	His
1			5				10				15				
Pro	Glu	Arg	Leu	Glu	Val	Ile	Asn	Glu	Ser	His	Gln	His	Thr	Gly	His
		20					25				30				
Gln	Pro	Gly	Phe	Asp	Gly	Thr	Gly	Glu	Ser	His	Met	Arg	Val	Arg	Ile
		35				40				45					
Val	Ser	Ser	Ala	Phe	Ala	Gly	Met	Ser	Arg	Val	Ala	Arg	His	Arg	Ala

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50	55	60
Ile Asn Asp Leu Leu Lys Pro Glu Leu Asp Ala Gly Leu His Ala Leu		
65	70	75
Ala Val Glu Pro Ala Ala Pro Gly Glu Pro Thr Arg Trp		
	85	90

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1017 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 - (A) ORGANISM: Pseudomonas denitrificans
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (ix) FEATURE:
 - (A) NAME/KEY: cobU
 - (B) LOCATION: 2099-3115 bp of SEQ ID NO: 30
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATGAGTGCCA	GCGGCCTGCC	GTTTGATGAT	TTTCGCGAAT	TGTTGCGCAA	CCTGCCGGGC	60
CCGGATGCGG	CAGCCCTCGT	TGCCGCGCGG	GAGCGGGACG	CCCAGCTGAC	GAAGCCGCCG	120
GGCGCGCTCG	GCCGCTCGA	GGAAATCGCC	TTCTGGCTCG	CCGCTGGAC	GGGCAAGGCG	180
CCGGTGGTCA	ACCGGCCGCT	GGTGGCGATC	TTTGCCGGCA	ACCACGGCGT	CACCCGCCAG	240
GGGGTGACCC	CGTTCCCCTC	ATCCGTCACC	GCACAGATGG	TCGAGAATTT	TGCCGCCGGT	300
GGCGCTGCGA	TCAACCATAT	CTGCGTCAGC	CACGACCTCG	GGCTGAAGGT	CTTCGACCTC	360
GCACTCGAAT	ACCCGACCGG	TGATATCACC	GAGGAAGCCG	CGCTGTCCGA	GCGCGATTGC	420
GCCGCGACCA	TGGCCTTTGG	CATGGAGGCG	ATTGCCGGCG	GCACGGATCT	TCTGTGCATC	480
GGCGAAATGG	GCATCGGCAA	CACCACGATC	GCGGCCGCGA	TCAATCTCGG	CCTTTATGGT	540
GGCACGGCCG	AAGAATGGGT	CGGTCCGGGT	ACCGGCTCCG	AGGGCGAGGT	GCTGAAGCGC	600
AAGATCGCCG	CGGTCGAAAA	GGCCGTGGCG	CTGCATCGCG	ATCACCTGTC	CGATCCGCTC	660
GAAGTATGTC	GTCGCCTCGG	CGGTCGTGAG	ATCGCGGCCA	TGGCTGGCGC	CATCCTGGCC	720
GCCCGCGTCC	AGAAGGTACC	TGTCATCATC	GACGGCTACG	TGGCGACCGC	TGCGGCTTCG	780
ATCCTGAAGG	CGGCCAACCC	GTCGGCCCTC	GACCATTGCC	TGATCGGCCA	TGTTTCGGGC	840
GAACCGGGGC	ATCTGCGCGC	GATCGAGAAG	CTCGGCAAGA	CGCCGCTGCT	GGCACTCGGC	900
ATGCGGCTTG	GCGAAGGCAC	GGGCGCGGCC	CTTGCCGCCG	GTATCGTCAA	GGCGGCGGCC	960
GCTTGCCACA	GCGGCATGGC	GACCTTTGCC	CAGGCCGGCG	TCAGCAACAA	GGAATAG	1017

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 amino acids
 - (B) TYPE: Amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBU
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Met	Ser	Ala	Ser	Gly	Leu	Pro	Phe	Asp	Asp	Phe	Arg	Glu	Leu	Leu	Arg
1				5					10					15	
Asn	Leu	Pro	Gly	Pro	Asp	Ala	Ala	Ala	Leu	Val	Ala	Ala	Arg	Glu	Arg
			20					25					30		
Asp	Ala	Gln	Leu	Thr	Lys	Pro	Pro	Gly	Ala	Leu	Gly	Arg	Leu	Glu	Glu
		35					40					45			
Ile	Ala	Phe	Trp	Leu	Ala	Ala	Trp	Thr	Gly	Lys	Ala	Pro	Val	Val	Asn
	50					55					60				
Arg	Pro	Leu	Val	Ala	Ile	Phe	Ala	Gly	Asn	His	Gly	Val	Thr	Arg	Gln
65					70				75					80	
Gly	Val	Thr	Pro	Phe	Pro	Ser	Ser	Val	Thr	Ala	Gln	Met	Val	Glu	Asn
				85					90				95		
Phe	Ala	Ala	Gly	Gly	Ala	Ala	Ile	Asn	Gln	Ile	Cys	Val	Ser	His	Asp
			100					105					110		
Leu	Gly	Leu	Lys	Val	Phe	Asp	Leu	Ala	Leu	Glu	Tyr	Pro	Thr	Gly	Asp
		115					120					125			
Ile	Thr	Glu	Glu	Ala	Ala	Leu	Ser	Glu	Arg	Asp	Cys	Ala	Ala	Thr	Met
	130					135					140				
Ala	Phe	Gly	Met	Glu	Ala	Ile	Ala	Gly	Gly	Thr	Asp	Leu	Leu	Cys	Ile
145					150				155					160	
Gly	Glu	Met	Gly	Ile	Gly	Asn	Thr	Thr	Ile	Ala	Ala	Ala	Ile	Asn	Leu
			165						170					175	
Gly	Leu	Tyr	Gly	Gly	Thr	Ala	Glu	Glu	Trp	Val	Gly	Pro	Gly	Thr	Gly
		180						185					190		
Ser	Glu	Gly	Glu	Val	Leu	Lys	Arg	Lys	Ile	Ala	Ala	Val	Glu	Lys	Ala
		195					200					205			
Val	Ala	Leu	His	Arg	Asp	His	Leu	Ser	Asp	Pro	Leu	Glu	Leu	Met	Arg
	210					215					220				
Arg	Leu	Gly	Gly	Arg	Glu	Ile	Ala	Ala	Met	Ala	Gly	Ala	Ile	Leu	Ala
225					230					235				240	
Ala	Arg	Val	Gln	Lys	Val	Pro	Val	Ile	Ile	Asp	Gly	Tyr	Val	Ala	Thr
			245						250					255	
Ala	Ala	Ala	Ser	Ile	Leu	Lys	Ala	Ala	Asn	Pro	Ser	Ala	Leu	Asp	His
			260					265					270		
Cys	Leu	Ile	Gly	His	Val	Ser	Gly	Glu	Pro	Gly	His	Leu	Arg	Ala	Ile
		275					280					285			
Glu	Lys	Leu	Gly	Lys	Thr	Pro	Leu	Leu	Ala	Leu	Gly	Met	Arg	Leu	Gly
	290					295					300				

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Glu	Gly	Thr	Gly	Ala	Ala	Leu	Ala	Ala	Gly	Ile	Val	Lys	Ala	Ala	Ala
305				310					315					320	
Ala	Cys	His	Ser	Gly	Met	Ala	Thr	Phe	Ala	Gln	Ala	Gly	Val	Ser	Asn
				325					330					335	

Lys Glu

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 909 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas denitrificans*
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (ix) FEATURE:
 - (A) NAME/KEY: cobV
 - (B) LOCATION: 1885-2793 bp of SEQ ID NO:30
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

ATGAAAGGTC	TGGGAAAGT	GTGCGCGCC	CTCGCGGGT	CGCCCGCCCG	GCTTGCGAGA	60
CTCGCCGAG	TGGCGAGTT	TGGCAGCGG	CGGGTCAAT	GCCGCAACCT	TGGAGGAGCC	120
ATGGGCTTC	TTGGCGATT	CTGTGACGAT	GTGGCGCGGT	CGATCGGCTT	TCTCAGCCGC	180
ATCCCGATGC	CTGCGCGTCA	TTTCGAAGGT	TATGACGGGC	GCTTGAGCCG	TGCCGTGCGC	240
GCCTTCCCGT	TCGCCGGCCT	GGCGATCGCA	CTGCCATCGG	CGGCCGTGCG	CATGGCCCTC	300
ATGGCGCTGC	AGGTGAGCTC	GCTCTTTGCC	GCCTTTGTCT	TCGTCGCCAT	CCAGGCGCTT	360
GTCACCGGCG	CACTGCACGA	AGACGGGCTT	GGCGACACGG	CCGATGGCTT	TGGCGGCGGT	420
CGCGACCGCG	AAGCGGCGCT	TGCGATCATG	AAGGACAGCC	GCATCGGCAC	CTATGCGGCC	480
GTCGCCCTCA	TCCTCTCCTT	CGGCCTGCGC	GTCTCGGCGT	TCGCCTCGAT	CCTGCCGCTC	540
TTTTCGCCGC	TGGGCGCCGC	CATGGCGATC	CTTGGCGCAG	CGTGCCTCAG	CCGCGCCGCC	600
ATGGTCTGGC	ACTGGTCGTC	GCTTCCGCCG	GCGCGCAGCA	GCGGCGTCGC	GGCCTCGGCT	660
GGCGAGCCGG	AACCGGCGGC	CACGCGCTTC	GCGCTTGCCT	TCGGACTTCT	TGTCGCAATG	720
CTGCTCTTCT	ATCTCGCGCA	GGTCCCGGCG	CTCGGCGTCA	TCGCGGCGCT	CGTCGCATTC	780
CTTGCCACGG	TCAAGGGCTT	CGCTCGGCTG	GCGATGCGCA	AGATCGGCGG	ACAAACGGGC	840
GACACGATCG	GGGCGACGCA	GCAACTGACC	GAAATCGCCG	TGCTCGGTGC	CCTTGCGCTG	900
ACGGTTTGA						909

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 302 amino acids
 - (B) TYPE: Amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBV
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

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Met Lys Gly Leu Gly Lys Val Cys Ala Ala Leu Ala Gly Ala Pro Ala
1      5      10      15
Arg Leu Ala Arg Leu Ala Ala Val Gly Glu Phe Gly Ser Gly Arg Val
20     25     30
Asn Gly Arg Asn Leu Gly Gly Ala Met Gly Phe Val Gly Asp Phe Cys
35     40     45
Asp Asp Val Ala Arg Ser Ile Gly Phe Leu Ser Arg Ile Pro Met Pro
50     55     60
Ala Arg His Phe Glu Gly Tyr Asp Gly Arg Leu Ser Arg Ala Val Arg
65     70     75     80
Ala Phe Pro Phe Ala Gly Leu Ala Ile Ala Leu Pro Ser Ala Ala Val
85     90     95
Ala Met Ala Leu Met Ala Leu Gln Val Ser Ser Leu Phe Ala Ala Phe
100    105    110
Val Val Val Ala Ile Gln Ala Leu Val Thr Gly Ala Leu His Glu Asp
115    120    125
Gly Leu Gly Asp Thr Ala Asp Gly Phe Gly Gly Gly Arg Asp Arg Glu
130    135    140
Ala Ala Leu Ala Ile Met Lys Asp Ser Arg Ile Gly Thr Tyr Ala Ala
145    150    155    160
Val Ala Leu Ile Leu Ser Phe Gly Leu Arg Val Ser Ala Phe Ala Ser
165    170    175
Ile Leu Pro Leu Phe Ser Pro Leu Gly Ala Ala Met Ala Ile Leu Gly
180    185    190
Ala Ala Cys Leu Ser Arg Ala Ala Met Val Trp His Trp Ser Ser Leu
195    200    205
Pro Pro Ala Arg Ser Ser Gly Val Ala Ala Ser Ala Gly Glu Pro Glu
210    215    220
Pro Ala Ala Thr Arg Phe Ala Leu Ala Phe Gly Leu Leu Val Ala Met
225    230    235    240
Leu Leu Phe Tyr Leu Ala Gln Val Pro Ala Leu Gly Val Ile Ala Ala
245    250    255
Leu Val Ala Phe Leu Ala Thr Val Lys Gly Phe Ala Arg Leu Ala Met
260    265    270
Arg Lys Ile Gly Gly Gln Thr Gly Asp Thr Ile Gly Ala Thr Gln Gln
275    280    285
Leu Thr Glu Ile Ala Val Leu Gly Ala Leu Ala Leu Thr Val
290    295    300

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(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13144 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Nucleotide Sequence of the 5' to 3'

strand from the 13144 bp SstI-SstI-SstI-SstI-BglII-BglII fragment of *Pseudomonas denitrificans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGCTCGAAG	GGGCTTCCGC	CCCGATCGCT	GGCGTTAGCC	GACGTTTCGAC	GTGCGGATGA	60
CGCCGAGCGG	GCCGAAGGGG	GCGTCGACGA	CGAGGTTGCG	TACGCGCGAC	TGGCTGGACG	120
GAACCTTCGA	GTTCCAGGCG	ATCTGAACGA	AATTGGGCTT	GCTGAAAATA	TACAGCATGG	180
ACATGAACCT	TGAGAGGCCG	GAGGCCTATC	CTCCGGGGCG	TGTTGCTATG	CCGCTGATAT	240
AGGTGTGCGC	TGCAAAAAAT	TGAATGCCAA	ACTCGCCACG	CCATGTCGCA	TTCTGGCTAT	300
CGGCCGCGAC	ATTTTCGACA	AGCCTTGCGA	AAGCGCGAAA	CAATGCGTGA	AAGGGCTTTG	360
TCAATTGCGG	CGAAATCGTG	TCGAAACAGA	CCTTTGCCCG	TGCCCCGTTT	AGTGTTACCG	420
ATGGCCGCAT	GACACGCAGG	ATCATGTTGC	AGGGAACCGG	CTCGGATGTC	GGAAAATCGG	480
TATTGGTGCG	GGGGCTCTGC	CGGCTTGCCG	CCAATCAGGG	CCTGAAGGTC	CGGCCGTTCA	540
AGCCGCAGAA	CATGTCGAAC	AACGCCGCGG	TTTCCGACGA	CGGCGGCGAG	ATCGGCCGCG	600
CGCAATGGCT	GCAGGCGCTG	GCCGCGCGCG	TGCCGTCGTC	GGTGACATG	AACCCGGTGC	660
TCCTGAAGCC	GCAGTCGGAC	GTGGGCAGCC	AGATCGTCGT	TCAGGGCAAG	GTCGCCGGGC	720
AGGCCAGGGG	GCGGGAATAT	CAGGCGCTCA	AGCCCAAGCT	GCTGGGCGCC	GTCATGGAGA	780
GTTTCGAACA	AATATCGGCC	GGTGCCGATC	TCGTGGTGGT	CGAAGGCGCC	GGCTCGCCGG	840
CCGAAATCAA	CCTCAGGCC	GGCGACATCG	CCAATATGGG	CTTTGCGACA	CGGGCCAATG	900
TGCCGGTCGT	GCTGGTCGGC	GACATCGACC	GCGGGGGGGT	GATCGCCTCG	CTGGTCGGCA	960
CGCATGCGAT	CCTGCCCGAG	GAAGACCGGC	GCATGGTGAC	CGGCTATCTC	ATCAACAAGT	1020
TCCGCGGCGA	CGTCACGCTG	TTGACGACG	GCATTGCTGC	CGTCAACCGC	TACACCGGCT	1080
GGCCCTGCTT	CGGCGTCGTG	CCGTGGCTGA	AGGCGGCGGC	ACGCCTGCCG	GCGGAAGATT	1140
CCGTGCTGCT	GGAGAAGCTG	ACGCGCGGGC	AGGGGCGGGC	GCTGAAGGTT	GCCGTCCCGG	1200
TACTGTGCGC	CATCGCCAAT	TTGACGACC	TCGATCCGCT	CGCCGCCGAA	CCGAGATTG	1260
ATCTCGTCTT	CGTGCGGCCT	GGCAGTCCCA	TTCCGGTCGA	CGCTGGCCTC	GTCGTCATT	1320
CCGGGTGCAA	ATCGACCATC	GGCGACCTCA	TCGATTTCCG	TGCGCAAGGG	TGGGACCGTG	1380
ACCTCGAACG	TCATGTGCGC	CGGGGCGGCC	GGGTCATCGG	CATCTGCGGC	GGCTACCAGA	1440
TGCTCGGCCG	GCGCGTCACC	GATCCGCTCG	GCATCGAGGG	CGGCGAACGT	GCGGTCGAGG	1500
GCCTCGGGCT	GCTCGAGGTC	GAGACCGAGA	TGGCGCCGGA	AAAGACGGTG	CGCAACAGCC	1560
GCGCCTGGTC	GCTGGAGCAT	GATGTGGTGC	TCGAAGGCTA	CGAAATCCAT	CTTGGAAGA	1620
CGCAAGGTGC	GGACTGTGGC	CGGCCGTCGG	TGCGCATCGA	CAATCGCGCC	GACGGCGCCC	1680

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TTTCGGCCGA	TGGCCGCGTG	ATGGGCACCT	ACCTGCATGG	GCTCTTCACC	AGCGACGCCT	1740
ATCGCGCGCG	GCTGCTCAAG	AGTTTCGGCA	TCAAGGCGG	CGCCAACAAC	TACCGCCAAT	1800
CGGTGCGATGC	GGCGCTCGAC	GATGTCGCGA	ACGAACTGGA	GGCTGTGCTC	GATCGTCGCT	1860
GGCTGGACGA	GTTGCTCAGG	CACTAGGGAC	GCGGCAACGG	TAGCCAGCA	GGTCCGGTAC	1920
GTCGGGCCCA	ACAGGAGCAA	CGAGCTTATC	CGACGGAAC	ACGCTGCGAC	ATCGTGCTCC	1980
TCGCTTGCGG	CTTCCCAGAC	TTCCCGCGCG	GCATCCAGGT	TCATCAGGGC	AATCCCCAGG	2040
CCGACGATCA	GGTCCGGCCA	GGCCGACTGC	CACAGATAGG	CTGTGCGCCAG	ACCCGCGGGC	2100
ATGATGGCCA	CATTGGCGAA	GGCATCGTTG	CGGGCCGAGA	GAAATGCTGC	CCGCGTGAGC	2160
GTGCCGCTCG	TGTGACGGTA	GGCGACGAGC	AGATAGGCGC	AGAAGAGGTT	GACCACCAGC	2220
GCCCCAAGTC	CGGTGAGGGA	CAGGGCAAAG	GGCTCTGGCG	GGACCGGATC	CATGAACTTC	2280
GCCCAGGCCG	TCCAAAGGAA	GGCCAGCGCC	GGTACCAGTA	GAATGAACGC	CATCGCCATG	2340
CCGACCCGCG	CGCGGGTTCG	CGCCGTCCAG	GCCAGAGCAA	AGAAAATCAG	CATGTTGACG	2400
GAGGCGTCTT	CGAGGAAGTC	GACGCTGTCT	GCCATGAGGG	ACACCGAGCC	GATCGAAAGC	2460
GCGACAAGGA	GTTTCGACCC	GAAATAGCCA	AGGTTCAACA	GGGAGACGAT	GAGGACGACG	2520
CGGCGCAGGT	CGGTATCCAC	TCGAAAGGTT	CCCTTTCTGG	CGAGATTTCG	CCTCGGCACT	2580
TTTTTTGGCG	AGATTGCCCC	TCGGCACTTT	GGCACAGGTG	TTAGCAGCAG	TTTGCTATCC	2640
ATAGCACTAG	GTTTCGACAT	CGGTTCCGTT	CACACTGCCG	TCGTGCCTGA	CGCCCGACAA	2700
ATCGTCGCGT	GGCGCAACTC	GGCCGGGGAG	GCGTCGCGATG	CGTCGATTGA	CTTTGGGCTG	2760
CCCGCTTCCT	AATCATCAGG	TGTTGGATGG	TTCCCCCTTG	TCGTGGCGAT	CTGGGGGAAT	2820
AATTGGGAAT	GTGACGGATG	GACCCAAATC	GGGCATCCTT	ATCGCAGCCG	ACCCGCGCAG	2880
TGTAGAACGG	TACAGGGTTC	CCATCGGGAT	TGGTCCGGGG	CTGTGCGCCG	GTTGCATGGG	2940
CAATCGGGGG	AGGTGCGGGG	TCAAGCCGGA	AAAGCCACTG	GCGTGGCATC	GTGATCAGCC	3000
GGGTTTGGAC	GCCTCTTCTT	CTACGAATCG	TCCGCCCTTT	ACGATGTCCC	TCACAGCGCC	3060
CATGCGTCGG	AGACGACGCG	CAAAGGTTTC	CTGTGGCACC	GGAAAGACGC	CGGGAAGGTG	3120
AGGCGGGCCG	CTCGGGCCCT	GACATCGGAA	CCTTGCCGTT	TAAGGGCGAG	GCGATGTTCT	3180
GCCCGTGACG	CCGTGAGCCA	GGAGACCTGC	CATCCGGCAT	GGGCATTCCG	CCCGAGGGGA	3240
CTTTTGTCTC	CAACGCCATC	ACGGAGGTTG	TTTTGGCTCG	CAGATGTTTT	CAAGAACGCG	3300
CCCGTGCGCG	GTCCGATGGC	TTTTGCCACC	GACGGCTGAT	TTGGGAATGT	TGAGGCAGCC	3360
ACGATGAGCA	GTCTCAGCGC	CGGGCCCCGT	CTGGTCCTTG	GCGGCGCCCG	TTCCGGCAAG	3420
TCCAGCTTTT	CCGAGAGGCT	CGTCGAAGCG	TCCGGCTTCA	CCATGCATTA	TGTCGCCACG	3480
GGCCGCGCCT	GGGACGACGA	AATGCGCGAG	GCGATCGACC	ATCACCAGAC	GCGCCGCGGC	3540
GAGGCGTGGG	CGACGCGATG	GGAGCCGCTC	GATCTCGTGC	GCATCCTCAG	ACGCATCGAT	3600
GATCCGAGCC	ATGTGGTCTT	GATCGACTGC	CTGACGCTAT	GGGTACCAA	TCTCATGTG	3660
GAAGAGCGCG	ACATGACGGC	GGAGTTTCGCC	GCCCTTGTTG	CGTATCTGCC	CGAGGCGCGG	3720
GCGCGCCTCG	TCTTTGTTTC	CAATGAGGTC	GGCCTCGGCA	TCGTGCCCGA	GAACCGCATG	3780
GCCCGCGAGT	TTCCGCGACCA	TGCCGGCCGG	CTTCACCAGA	TCGTTGCGGA	GAAATCCGCT	3840
GAAGTTTACT	TTGTGCGCGG	CGGTTTGCCG	CTGAAAATGA	AGGGTTGATC	CATGACCACT	3900
GCGAGAGCCA	ACCAGGGCAA	GATCCCGGCG	ACCGTCATCA	CCGGCTTCCT	CGGCGCCGGC	3960
AAGACGACGA	TGATCCGCAA	CCTGCTCGAG	AACGCCGACG	GCAAGCGCAT	CGGCCTGATC	4020
ATCAACGAGT	TCGGCGATCT	TGGCGTCGAC	GGCGATGTCT	TGAAGGGCTG	CGGTGCCGAG	4080
GCCTGCACCG	AGGACGACAT	CATCGAGCTC	ACCAATGGCT	GCATCTGCTG	CACCGTGGCT	4140
GACGATTTCA	TCCCCAGCAT	GACGAAGCTG	CTCGAGCGTG	AAAACCGTCC	TGACCACATC	4200
ATCATCGAAA	CCTCGGGCCT	TGCCCTGCCG	CAGCCGCTGA	TCGCCGCTTT	CAACTGGCCG	4260
GATATCCGCA	GCGAAGTGAC	CGTCGATGGC	GTGTCACCG	TGGTCGACAG	CGCCGCCGTT	4320
GCCGCTGGCC	GCTTTGCCGA	CGACCACGAC	AAGGTCGATG	CGCTGCGCGT	CGAGGACGAT	4380
AATCTCGATC	ACGAAAGCCC	GATCGAGGAG	CTGTTTCGAG	ATCAACTGAC	GGCTGCCGAT	4440
CTCATCGTTC	TCAACAAGAC	CGATCTGATC	GATGCCTCCG	GCCTCAAGGC	CGTGCGCGAC	4500
GAGGTGTCTT	CGCGCACCAG	CCGCAAGCCC	ACGATGATCG	AGGCGAAAAA	CGGCGAAGTC	4560
GCCGCTGCCA	TCCTGCTTGG	CCTCGGTGTC	GGCACGGAAA	GCGATATCGC	CAACCGCAAG	4620
TCGCATCAGC	AGATGGAGCA	CGAGGCAGGT	GAGGAGCAGC	ATCACGACGA	GTTGACAGC	4680
TTGCTGCTCG	AGCTCGGTTT	GATCGCCGAT	CCGGCCGCTT	TCATCGATCG	CCTGAAGGGC	4740
GTAATCGCGG	AGCACGACGT	TCTGCGCCTC	AAGGGTTTTG	CAGACGTGCC	CGGCAAGCCG	4800
ATGCGCCTCC	TGATCCAGGC	GGTCGGCGCC	GCGATCGACC	AATATTACGA	CCGCGCCTGG	4860
GGCGCTGGCG	AAAAGCGCGG	TACGCGCCTC	GTCGTCATCG	GCCTGCACGA	CATGGACGAG	4920
GCGGCGGTGC	GCGCCGCGAT	CACCGCGCTC	GTGTAGATCT	TTCTTTGAAT	GAAATGATCT	4980
AACGCAATTGA	AATGATGCAG	TTCCGGATGG	AGAACGCTTT	TAGCGTTTTT	GTTGGAATT	5040
GCCCCAATCG	ACAAGACGAA	TGCATCTGCT	TCTCGCCGAG	AAAGGAACGA	TCGCCGACGG	5100
CAACGAGGCG	ATCGACCTTG	GGCAAACGCC	GGCCGATATC	CTTTTCTAT	CGGCCGCCGA	5160
CACCGAGCTC	TCCTCGATCG	CCGCGGCTCA	CGGCCGACGC	GACGGAGGCT	TGAGCCTGCG	5220
CATCGCCAGC	CTGATGAGCC	TGATGCACCC	GATGTCGGTC	GACACTTACG	TCGAGCGCAC	5280
GGCGCGTCAC	GCCAAGCTGA	TCGTGCTCCG	GCCGCTCGGT	GGCGCCAGCT	ATTTCCGTTA	5340
TCTGCTGGAA	GCCCTGCATG	CGGCTGCCGT	CACCCATCGT	TTGAGATCG	CGGTTCTGCC	5400
GGGTGACGAC	AAGCCGGATC	CGGGGCTGGA	GCCTTTCTCC	ACCGTCGAG	CCGACGACCG	5460

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CCAGCGCCTT	TGGGCTTACT	TCACCGAAGG	CGGCTCGGAC	AATGCCGGGC	TGTTTCTCGA	5520
CTATGCGGCC	GCACTGGTCA	CAGGTGCGGA	GAAGCCGCAG	CCGGCAAAGC	CCCTGTTGAA	5580
GGCCGGCATC	TGGTGGCCGG	GTGCTGGTGT	GATCGGCGTC	AGCGAATGGC	AGTCCCTTGT	5640
TCAGGGACGG	ATGGTAGCGA	GGGAGGGATT	CGAACCCCGG	ACGGTCGGGA	TCTGCTTTTA	5700
CCGCGCGCTC	GTGCAGAGTG	GCGAGACACG	GCCTGTGGAG	GCGCTGATCG	ATGCGCTGGA	5760
GGCTGAAGGT	GTGCGGGCAC	TGCCGGTGTT	TGTCTCAAGC	CTCAAGGATG	CCGTTTCCGT	5820
CGGCACGCTG	CAGGCGATTT	TTTCCGAGGC	CGCACCCGAC	GTGGTGATGA	ACGCCACTGG	5880
CTTTGCGGTC	TCGTGCCCCG	GTGCCGACCG	TCAGCCGACG	GTGCTGGAAT	CGACCGGTGC	5940
GCCGGTGCTG	CAGGTGATTT	TCTCCGGCTC	GTGCGGGGCG	CAATGGGAAA	CGTCGCCGCA	6000
GGGGCTGATG	GCGCGCGACC	TCGCCATGAA	CGTGGCACTC	CCCGAAGTCG	ATGGCCGCAT	6060
CCTTGCGCGC	GCCGTCTCCT	TCAAGGCGGC	GTCGATCTAT	GACGCCAAGG	TGGAGGCCAA	6120
TATCGTCGGC	CATGAGCCGC	TCGAAGGCCG	GGTGCGCTTT	GCCGCTGATC	TTGCCGTCAA	6180
CTGGGCGAAC	GTGCGCCGGG	CAGAGCCCGC	CGAGCGCCGT	ATTGCCATCG	TCATGGCCAA	6240
CTATCCGAAC	CGCGACGGTC	GCCTCGGCAA	CGGTGTGCGG	CTCGACACGC	CGGCCGGTAC	6300
CGTCGAGGTG	CTTAGCGCCA	TGGCGCGGGA	AGGCTATGCG	GTGCGTGAGG	TTCCCGCCGA	6360
TGGCGACGCG	CTGATCCGCT	TTCTGATGGC	CGGGCCGACC	AATGCGGCGA	GCCATGACCG	6420
TGAAATCCGC	GAGCGTATTT	CGCTGAACGA	TTACAAAACG	TTCTTCGATT	CGTTTCCGAA	6480
ACAGATAAAG	GATGAAGTTG	CCGGTCGCTG	GGGCGTGCCG	GAGGCCGATC	CCTTTTTTCT	6540
CGATGGCGCC	TTGCGGCTCG	CGCTCGCCCC	CTTCGGCGAG	GTGATCGTCG	GCATCCAACC	6600
GGCGCGCGGC	TACAACATCG	ATCCGAAGGA	AAGCTACCAT	TCCCGGACC	TCGTGCCGCC	6660
GCATGGCTAT	CTCGCCTTCT	ACGCCTTCT	GCGCCAGCAG	TTCCGAGCGC	AGGCGATCGT	6720
CCACATGGGC	AAGCACGGCA	ATCTCGAATG	GCTGCCGGGC	AAGGCGCTGG	CGCTGTGCGA	6780
AACCTGCTAT	CCCGAAGCGA	TCTTCGGGCC	GCTGCCGCAC	ATCTATCCCT	TCATCGTCAA	6840
CGATCCGGGC	GAAGGTACGC	AGGCCAAGCG	CCGCACCAGC	GCCGTATCA	TCGACCACCT	6900
GACCCCGCCC	TTGACGCGCG	CCGAATCCTA	CGGCCCGCTC	AAGGATCTGG	AAGCGCTCGT	6960
CGACGAATAT	TACGACGCGC	CCGGCGGTGA	TCCGCGCCGC	CTCAGGCTGC	TCAGCCGCCA	7020
GATCCTCGAT	CTCGTGCCGC	ACATCGGCCG	GCACAGCGAC	GCAGGCATCG	ACAGGGGCGA	7080
CAGCGACGAC	AAGGCGCTGG	AAAAGCTCGA	CGCCTATCTC	TGCGACCTCA	AGGAAATGCA	7140
GATCCGCGAC	GGCCTGCACA	TCTTCGGCGT	TGCGCCGGAA	GGGCGTTGT	TGACGGACCT	7200
CACCGTAGCG	CTGGCGCGCG	TGCCCCGAGG	TCTCGGCGAG	GGCGGCGACC	AGAGCCTGCA	7260
GCGGGCGATC	GCAGCGGATG	CGGGGCTGCG	TGGGTTTGCT	ATTCCCACCT	CGGCGGGGGG	7320
CAACCCCGCA	CGCGACGCCC	AACCCCTTCA	CCCGCTCGAC	TGCGTCATGT	CCGACACCTG	7380
GACAGGCCCC	AAACCGTCCA	TCCTCGTGTA	CCTCTCGGAC	GCCCCCTGGC	GCACCGCCGG	7440
CGATACGGTC	GAGCGCATCG	AGTTGCTTGC	CGCAAATCTC	GTGTGCGGTG	AACTGGCTTG	7500
CCCGGACCAC	TGGGCCAACAA	CCCGCGCCGT	GCTCGGCGAA	ATCGAAACGC	GCCTGAAGCC	7560
GTGATTTTCA	AACTCGGGTG	CCGCCGAGAT	GACCGGCTTC	CTCACCGGTC	TCAGCGGCCG	7620
CTTCGTGCGC	CCCGGTCCAT	CGGGCGCGCC	GACGCGCGGC	CGGCCGGATG	TGTTGCCGAC	7680
GGGGCGCAAT	TTCTACTCGG	TCGACAGCCG	CGCGTGCCG	ACGCCGGCGG	CTTACGAGCT	7740
TGGCAAGAAA	TCGGCCGAGC	TTCTGATCCG	CCGCTACCTG	CAGGACCATG	GCGAATGGCC	7800
GTCTCTCTTT	GGCCTGACCG	CCTGGGGCAC	GGCGAACATG	CGCACCGGCG	GCGACGACAT	7860
CGCCCAGGCC	CTGGCGCTGA	TCGGCGCCAA	GCCCACCTGG	GACATGGTCT	CTCGCCGGGT	7920
GATGGGCTAC	GAGATCGTGC	CGCTCGCAGT	CCTCGGCCGC	CCACGCGTCG	ACGTGACCTT	7980
GCGCATTTCC	GGCTTCTTCC	GCGATGCCTT	CCCGGACCAG	ATCGCGCTCT	TCGACAAGGC	8040
GATCCGCGCC	GTCGCGCTGG	AGGAAGACGA	TGCCGACAAC	ATGATCGCCG	CACGCATGCG	8100
GGCGGAAAGC	CGCCGGCTGG	AGGCCGAAGG	CGTGGAAGCC	GCCGAGGCCG	CGCGTCGCGC	8160
CTCCTACCGC	GTCTTTGGCG	CAAAGCCCGG	TGCCTATGGC	GCCGCCCTGC	AGGCGCTGAT	8220
CGACGAGAAG	GGCTGGGAAA	CCAAAGCAGA	TCTCGCCGAG	GCCTATCTTA	CCTGGGGCGC	8280
CTATGCCTAT	GGCGCCGGCG	AGGAGGGCAA	GGCCGAGCGC	GATCTTTTCG	AGGAGCGCCT	8340
GCGCACGATA	GAGGCGGTGG	TGCAGAACCA	GGACAACCGC	GAGCACGATC	TGCTCGACAG	8400
CCAGCACTAC	TACCAGTTTC	AAGGCGGCAT	GAGCGCTGCC	GCCGAACAGC	TCGGCGGTCA	8460
CCGTCCGGCG	ATCTACCACA	ACGACCATTTC	CCGTCCGGAA	AAGCCTGTGA	TCCGGTCGCT	8520
CGAAGAAGAG	ATCGGCCGCG	TGGTCCGGGC	CCGCGTCGTC	AATCCCAAGT	GGATCGATGG	8580
CGTCATGCGC	CACGGATACA	AGGGCGCCTT	CGAGATCGCT	GCCACGGTCG	ACTACATGTT	8640
CGCCTTTGCC	GCGACCACGG	GTGCGGTGCG	CGACCATCAT	TTGAGGGCCG	CTTATCAGGC	8700
GTTGATTGTC	GACGAGCGCG	TGGTGACTTT	CATGCGCGAC	AAGAACCCGG	CCGCCTTTGC	8760
CGAGCTTGCC	GAACGCTTGC	TTGAAGCAAT	CGACCGCAAT	CTCTGGACGC	CGCGCTCGAA	8820
TTGCGGCGCG	TTTGAACATTG	CCGGCATCGG	CACGGCAGCA	ACCCGGCTTC	GTGCCGGCAA	8880
TGAATAGAGC	GGTTCGGGGC	TGGCGGTTAT	CCGTCCGGAA	TTGCTTGGA	ACAAAGACCT	8940
GGTTCCGTTT	CGCTGCTCAG	TGAAGTGCGA	AAAGGAACCG	AAGCGGGACG	AGGGCGTCTG	9000
CCCATCCCCG	ACTTGAGAAC	TGAGGGAGTG	ATCATGAGCG	ACGAGACGAC	AGTAGGCGGC	9060
GAAGCCCCGG	CCGAGAAGGA	CGATGCCCGC	CACGCCATGA	AGATGGCGAA	GAAGAAGGCA	9120
GCACGCGAAA	AGATCATGGC	GACGAAGACC	GACGGAAGAG	GTCTGATCAT	CGTCAACACC	9180
GGCAAAGGCA	AGGGCAAGTC	GACCGCCGGC	TTCGGCATGA	TCTTCCGCCA	TATCGCCAC	9240

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GGCATGCCCT	GCGCCGTCGT	GCAGTTCATC	AAGGGTGCGA	TGGCAACCGG	CGAGCGCGAG	9300
TTGATCGAGA	AGCATTTTCG	CGATGTCTGC	CAGTTCTACA	CGCTCGGCGA	GGGCTTCACC	9360
TGGGAAACGC	AGGATCGCGC	CCGCGATGTT	GCGATGGCTG	AAAAGGCCTG	GGAGAAGGCG	9420
AAGGAACTGA	TCCGTGACGA	GCGCAACTCG	ATGGTGCTGC	TCGACGAGAT	CAACATTGCT	9480
CTGCGCTACG	ACTACATCGA	CGTCGCCGAA	GTGGTGCGCT	TCCTGAAGGA	AGAAAAGCCG	9540
CACATGACGC	ATGTGGTGCT	CACCGGCCGC	AACGCGAAAG	AAGACCTGAT	CGAAGTCGCC	9600
GATCTCGTCA	CTGAGATGGA	GCTGATCAAG	CATCCGTTCC	GTTCCGGCAT	CAAGGCGCAG	9660
CAGGGCGTGG	AGTTCTGATG	AGCCAGAGCT	GGCAGTTCTG	GGCGCTGCTT	TCGGCCGCCT	9720
TCGCTGCGCT	CACGGCGGTG	TTTGCCAAGG	TCGGGGTTGC	GCAGATCAAC	TCCGACTTCG	9780
CAACGCTGAT	CCGCACCGTC	GTCATCCTCT	GCGTGATCGC	CGCCATCGTG	GCGGCGACAG	9840
GGCAGTGGA	GAAGCCATCG	GAAATCCCGG	GCCGCACCTG	GCTGTTCTTG	GCGCTGTCAG	9900
GGCTTGCGAC	TGGCGCTTCC	TGGCTTGCTT	ATTTCCGCGC	GCTGAAGCTC	GGCGACGCCG	9960
CCCGCGTGGC	GCCGCTCGAC	AAGCTCTCGA	TCGTATGGT	CGCGATCTTC	GGCGTGCTCT	10020
TCCTCGTTGA	AAAGCTCAAC	CTGATGAAT	GGCTCGGCGT	CGCTTCATT	GCCGCCGGGG	10080
CGCTGTTGCT	GGCGGTGTTT	TGAGCGCGCC	TGCTCTGGTG	CCTGTTCACT	GAATGCTCGC	10140
CTCAATCAAT	CCGTAATCCC	GACACATGCA	GTGGTTGTGA	CGAGCGGGAG	GACGGCATGC	10200
AGATTGAAGG	CAATTGGAGC	GAGCGCCTTC	CTGATCCGTC	GGGCCACGTC	GCGCAGTTCTG	10260
GCAGACGCTG	GAAGCGTCGC	AGCCTGAGGG	TGAGCCCTGC	TTGAGACCCA	CCGGCGGACA	10320
CGCCTGCAAT	AGGCACCGTA	GGCGTCGCCG	AAGACCTTGG	CGAGGTGGGT	TTCTCTCCATG	10380
CGGATCTGGT	AGGAAATCGA	GATCCAGGCG	GAGAGCGCCA	GCGCCACCGA	GATGACGTTG	10440
GGCACCGCCA	TCACCGTGCC	GATCAGCGCG	GTCACCATGC	CGACATAGAT	CGGGTTGCGC	10500
GAGAAGGCAT	AGAGGCCTGA	GGTCACAAGC	GGCGCGTCCT	GCTTTTCAGG	GATGCCGATC	10560
TTCCAGGAAT	GACGCATCGC	CCATTGCGAC	AGCATCGTCA	GCCCGCCGCC	GAGCGTCATC	10620
AGCGCCAGGC	CGACGGCGTG	AAGGATGGGC	GTGTCGAGCG	CCGGGATCCG	GCCGAGGGCA	10680
GCATCGACGG	AGGCCGGGAG	CATGGCGACC	GCCAGCAGGT	GGATCACCAG	CGCTGCGACG	10740
ATCAGGCGGA	AAAGCTGCC	CGCAAACCTT	TCCGCATCGT	CGCCATAGGT	TAGCACGACC	10800
GGCGAGCGGC	CGGATTGCAC	GCGGCGGAGG	ATCGCCAGCG	CGAGCGTGGA	CAATCCCACG	10860
ACGAGCATCA	GGATGGTGGG	AAGGGTGGTG	GACATGGAAA	CCTCTGGAGC	GAGCTGACAA	10920
GACAGGAGCG	CACGACGGGT	AGGCGGCCCA	TATGAGCGTC	TACCCGGCGA	AGCATTCTGA	10980
TCACCTTGCA	ATCTCTAGTA	ACTAGAGGTT	CAAGCGTCGG	ACCTGTCCGA	CTTTCGTCGT	11040
GGTTACCGGA	TCTTATTGCC	AAGCGTTGGA	GGCTGTCACT	GTGCCCCCGG	CCGTGTCCGA	11100
AGGTCCGGCA	AATTCGTCTC	TTGACGGCTG	CTCCTTCCGT	CGAGCGATTG	CATAGCGAGG	11160
AGGCCGCACC	CATGTTAGAC	CGTCGACAGG	CTAAATACCG	GTGAACCTTG	AAGAATACTC	11220
TCAGAGCTGC	GGTTGGTGTC	GCATCGGTCT	TGCTGTTCTT	GTGATCAGGT	GTGGCGGGGC	11280
AGGCGCAAAC	CGTGAAGAGC	GGGGCGTCAC	GAGCTCAAGA	AACGACGACC	ACCCAGAAGG	11340
CGAAACCGAA	AACTAAAACG	ACGCGCAAGC	AAAGGGCTGC	GGATGAAGCC	AAGGCCAAGG	11400
CGCTCGCCGA	AGCGCGCCGT	CCACGGATTT	GCAAGACGCG	GGAGAGCGAA	TGCAGCTATG	11460
GCGCAGGTCC	GGTCGGAGAG	CAGTGCTCGT	CTGTGTCGAA	ATCCGGTGCG	CCTGATCTTG	11520
GCATAACTGT	CAGGCGTTGA	CCGCCCGCGA	CCTTCGCGCG	GGCAGGCAAG	CGTGCGTTCG	11580
TCGAAGCGAC	GCCTGACGCG	ATAGAAATCA	CGGGTCGCCT	GGTTGTTTCT	GAAAGCTTGG	11640
GATTGGGTTT	AGGTGATGGA	AGCCGGCGTT	GAACGCAAAA	TAATGATCGA	TCTCGAGAAC	11700
AGCGCGCTCC	AGTTTGCAAC	CCGAGCACAC	GGCGAACAGA	AGCGTAAGTA	TGACGGTCGG	11760
CCATATATCG	TTCATCCGAT	TGCGGTGGCG	GAGATTGTTT	GAAGCGTGCC	CCATACGCC	11820
GAAATGATCG	CCGACGCGCT	GCTTCACGAT	ACGGTCGAAG	ATACCGACGC	GACGCTGCTG	11880
GAGATCAAGG	AAGCGTTTCG	CCCCAAGGTC	GCAACACTGG	TTGCGTGGCT	CACCGACATA	11940
TCCACTCCGT	TCCACGGCAA	CCGACAGGTG	CGCAAGGAAC	TGGATCGCCA	GCACCTCGCA	12000
TCGGCGCCCC	CCGCGGCGAA	AACCGTCAAG	CTCGCCGACC	TGATCGACAA	TGCGATAGCG	12060
ATCAAAGCCG	GCGATCCGAA	TTTCTGGAAA	GTGTTCCGGC	CCGAGATGAA	ACGCTTGCTG	12120
GAGGTCTTGG	GCGACGGCGA	CGAGACCCTT	CTCGCAAAGG	CCCCTGCATT	AGCGCCGGAA	12180
TGAGAGTGCC	GCCGTTTATC	GGCAAGCATG	TCTGTGCCAT	GTGACCCCGG	TCAACCGGTC	12240
ATCCAAGATC	GCAGAACGGA	CATGCATTTG	CGGTTTTGCC	CGCCGGTGTC	GCCCAGCCAC	12300
GCCTCACAGG	CTGCGCGGTT	GCGGCCGTTA	GGACAGCGCA	GAATTTGCCG	ACCGCGCCGC	12360
GCCTCAATGC	CCCAGCCAGA	TCCGCAAGGG	ATGCGTCGGA	TCTGCGAGCA	GCCGGATCGC	12420
GAGCGCGATC	GAGACGATGA	CGAGCAGCGG	CTTGATGATC	TTGGCGCCCT	TGGCCATGGC	12480
ATAGCGCGAG	CCGACCTGGG	CGCCGAGGAA	CTGGCCGAGG	CCCATCAACA	GGCCGACCTT	12540
CCAGAGAACG	GCGCCGAAGA	AGAGGAAGAC	CCGGAAGGCG	CCGACGTTGG	AGCCAAAGTT	12600
GAGGAACTTC	GTGTGCGCCG	TCGCCTTCAA	CACGCCGAAG	CCGGCGAGGG	TAACGAAGCC	12660
GAGCATGAAG	AACGAGCCGG	TGCCGGGGCC	GAAGACGCCG	TCATAAAAGC	CGATTAGCGG	12720
CACCAAGTGC	AGCGTGAAGA	CGAAGGGGGT	GACGCGGCTG	TGCTGGTCTGA	CGTCGCCCAT	12780
GTTCCGGCTTC	AGGCCGAAAT	AAAGCGCAAT	GGCGATCAGC	AGAAAGGGCA	GGATCGCCTT	12840
CAGCAGCTGC	CCGGGAACGA	TGGTTGCGAG	CAGGGCGCCG	AGCACGGCGC	CGGCGGCCGA	12900
CATCAGCGCC	ATCGGCAGCT	GCTCTTTTCA	GTTACGCTGG	CCGCGCCGGG	CATAGGACAT	12960
CGTGGCCGAG	CCGGAGCCGA	ACAATCCCTG	CAGCTTGTTG	GTGCCGAGCG	TCTGCAAGGG	13020

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CGGGATGCCC	GCAATGAGCA	TGGCCGGAAT	GGTGATCATG	CCACCGCCGC	CGGCGATCGA	13080
ATCGATGAAG	CCTGCGATGA	AGGCGGCGAC	GAACAGGAAG	GCGAGCAGGT	GGAAGGCGAG	13140
ATCT						13144

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1458 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas denitrificans*
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (ix) FEATURE:
 - (A) NAME/KEY: cobQ
 - (B) LOCATION: 429-1886 bp of SEQ ID NO:41
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

ATGACACGCA	GGATCATGTT	GCAGGGAACC	GGCTCGGATG	TCGGAAAATC	GGTATTGGTG	60
GCGGGGCTCT	GCCGGCTTGC	CGCCAATCAG	GGCCTGAAGG	TCCGGCCGTT	CAAGCCGCAG	120
AACATGTCGA	ACAACGCCGC	CGTTTCCGAC	GACGGCGGCG	AGATCGGCCG	CGCGCAATGG	180
CTGCAGGCGC	TGGCCGCGCG	CGTGCCGTCG	TCGGTGCA	TGAACCCGGT	GCTCCTGAAG	240
CCGCAATCGG	ACGTGGGCAG	CCAGATCGTC	GTTTCAGGGA	AGGTCGCCCG	GCAGGCCAGG	300
GGGCGGGAAT	ATCAGGCGCT	CAAGCCCAAG	CTGCTGGGCG	CCGTCATGGA	GAGTTTCGAA	360
CAAATATCGG	CCGGTGCCGA	TCTCGTGGTG	GTGGAAGGCG	CCGGCTCGCC	GGCCGAAATC	420
AACCTCAGGC	CCGGCGACAT	CGCCAATATG	GGCTTTGCGA	CACGGGCCAA	TGTGCCGGTC	480
GTGCTGGTCG	GCGACATCGA	CCGCGGGGGG	GTGATCGCCT	CGCTGGTCGG	CACGCATGCG	540
ATCCTGCCCC	AGGAAGACCG	GCGCATGGTG	ACCGGCTATC	TCATCAACAA	GTTCCGCGGC	600
GACGTCACGC	TGTTTCGACG	CGGCATTGCT	GCCGTCAACC	GCTACACCGG	CTGGCCCTGC	660
TTCCGGCGTC	TGCCGTGGCT	GAAGGCGGCG	GCACGCCTGC	CGGCGGAAGA	TTCCGTCGTG	720
CTGGAGAAGC	TGACGCGCGG	CGAGGGGCGG	GCGCTGAAGG	TTGCCGTCCC	GGTACTGTCT	780
CGCATCGCCA	ATTTTCGACG	CCTCGATCCG	CTCGCCGCGG	AACCGGAGAT	TGATCTCGTC	840
TTCTGTCGGC	CTGGCAGTCC	CATTCCGGTC	GACGCTGGCC	TCGTCGTCAT	TCCCGGGTCG	900
AAATCGACCA	TCGGCGACCT	CATCGATTTT	CGTGCGCAAG	GGTGGGACCG	TGACCTCGAA	960
CGTCATGTGC	GCCGGGGCGG	CCGGGTCATC	GGCATCTGCG	GCGGCTACCA	GATGCTCGGC	1020
CGGCGCGTCA	CCGATCCGCT	CGGCATCGAG	GGCGGCGAAC	GTGCGGTCGA	GGGCCTCGGG	1080
CTGCTCGAGG	TCGAGACCGA	GATGGCGCGG	GAAAAGACGG	TGCGCAACAG	CCGCGCCTGG	1140
TCGCTGGAGC	ATGATGTGGT	GCTCGAAGGC	TACGAAATCC	ATCTTGGA	GACGCAAGGT	1200
GCGGACTGTG	GCCGGCCGTC	GGTGCGCATC	GACAATCGCG	CCGACGGCGC	CCTTTTCGGCC	1260
GATGGCCGCG	TGATGGGCAC	CTACCTGCAT	GGGCTCTTCA	CCAGCGACGC	CTATCGCGGC	1320
GCGCTGCTCA	AGAGTTTCGG	CATCGAAGGC	GGCGCCAACA	ACTACCGCCA	ATCGGTCGAT	1380
GCGGCGCTCG	ACGATGTGCG	GAACGAAGTG	GAGGCTGTGC	TCGATCGTCG	CTGGCTGGAC	1440
GAGTTGCTCA	GGCACTAG					1458

(2) INFORMATION FOR SEQ ID NO: 43:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 485 amino acids
 (B) TYPE: Amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 (A) ORGANISM: *Pseudomonas denitrificans*
 (B) STRAIN:
 (C) INDIVIDUAL ISOLATE:
 (D) DEVELOPMENTAL STAGE:
 (E) HAPLOTYPE:
 (F) TISSUE TYPE:
 (G) CELL TYPE:
 (H) CELL LINE:
 (I) ORGANELLE:
- (ix) FEATURE:
 (A) NAME/KEY: COBQ
 (B) LOCATION:
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION: Translation product of SEQ ID NO:42
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

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Met Thr Arg Arg Ile Met Leu Gln Gly Thr Gly Ser Asp Val Gly Lys
1      5      10      15
Ser Val Leu Val Ala Gly Leu Cys Arg Leu Ala Ala Asn Gln Gly Leu
20     25     30
Lys Val Arg Pro Phe Lys Pro Gln Asn Met Ser Asn Asn Ala Ala Val
35     40     45
Ser Asp Asp Gly Gly Glu Ile Gly Arg Ala Gln Trp Leu Gln Ala Leu
50     55     60
Ala Ala Arg Val Pro Ser Ser Val His Met Asn Pro Val Leu Leu Lys
65     70     75     80
Pro Gln Ser Asp Val Gly Ser Gln Ile Val Val Gln Gly Lys Val Ala
85     90     95
Gly Gln Ala Arg Gly Arg Glu Tyr Gln Ala Leu Lys Pro Lys Leu Leu
100    105    110
Gly Ala Val Met Glu Ser Phe Glu Gln Ile Ser Ala Gly Ala Asp Leu
115    120    125
Val Val Val Glu Gly Ala Gly Ser Pro Ala Glu Ile Asn Leu Arg Pro
130    135    140
Gly Asp Ile Ala Asn Met Gly Phe Ala Thr Arg Ala Asn Val Pro Val
145    150    155    160
Val Leu Val Gly Asp Ile Asp Arg Gly Gly Val Ile Ala Ser Leu Val
165    170    175
Gly Thr His Ala Ile Leu Pro Glu Glu Asp Arg Arg Met Val Thr Gly
180    185    190
Tyr Leu Ile Asn Lys Phe Arg Gly Asp Val Thr Leu Phe Asp Asp Gly
195    200    205
Ile Ala Ala Val Asn Arg Tyr Thr Gly Trp Pro Cys Phe Gly Val Val
210    215    220
Pro Trp Leu Lys Ala Ala Ala Arg Leu Pro Ala Glu Asp Ser Val Val
225    230    235    240
Leu Glu Lys Leu Thr Arg Gly Glu Gly Arg Ala Leu Lys Val Ala Val
245    250    255
Pro Val Leu Ser Arg Ile Ala Asn Phe Asp Asp Leu Asp Pro Leu Ala
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260	265	270
Ala Glu Pro	Glu Ile Asp Leu Val Phe Val Arg Pro	Gly Ser Pro Ile
Pro Val Asp	Ala Gly Leu Val Val Ile Pro Gly Ser	Lys Ser Thr Ile
Gly Asp Leu	Ile Asp Phe Arg Ala Gln Gly Trp Asp Arg	Asp Leu Glu
Arg His Val	Arg Arg Gly Gly Arg Val Ile Gly Ile Cys Gly	Gly Tyr
Gln Met Leu	Gly Arg Arg Val Thr Asp Pro Leu Gly Ile	Glu Gly Gly
Glu Arg Ala	Val Glu Gly Leu Gly Leu Leu Glu Val	Glu Thr Glu Met
Ala Pro Glu	Lys Thr Val Arg Asn Ser Arg Ala Trp Ser	Leu Glu His
Asp Val Val	Leu Glu Gly Tyr Glu Ile His Leu Gly Lys	Thr Gln Gly
Ala Asp Cys	Gly Arg Pro Ser Val Arg Ile Asp Asn Arg	Ala Asp Gly
Ala Leu Ser	Ala Asp Gly Arg Val Met Gly Thr Tyr Leu	His Gly Leu
Phe Thr Ser	Asp Ala Tyr Arg Gly Ala Leu Leu Lys Ser	Phe Gly Ile
Glu Gly Gly	Ala Asn Asn Tyr Arg Gln Ser Val Asp Ala	Ala Leu Asp
Asp Val Ala	Asn Glu Leu Glu Ala Val Leu Asp Arg	Arg Trp Leu Asp
Glu Leu Leu	Arg His	

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: cobP
- (B) LOCATION: 3364-3888 bp of SEQ ID NO:41
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

ATGAGCAGTC	TCAGCGCCGG	GCCCGTGCTG	GTCCTTGGCG	GCGCCCGTTC	CGGCAAGTCC	60
AGCTTTTCCG	AGAGGCTCGT	CGAAGCGTCC	GGCTTACCA	TGCATTATGT	CGCCACGGGC	120
CGCGCCTGGG	ACGACGAAAT	GCGCGAGCGC	ATCGACCATC	ACCGGACGCG	CCGCGGCGAG	180
GGCTGGACGA	CGCATGAGGA	GCCGCTCGAT	CTCGTCGGCA	TCCTCAGACG	CATCGATGAT	240
CCCAGCCATG	TGGTCCTGAT	CGACTGCCTG	ACGCTATGGG	TCACCAATCT	CATGCTGGAA	300
GAGCGCGACA	TGACGGCGGA	GTTTCGCCGC	CTTGTTGCGT	ATCTGCCCCG	GGCGCGGGCG	360
CGCCTCGTCT	TTGTTTCCAA	TGAGGTCGGC	CTCGGCATCG	TGCCCCGAGAA	CCGCATGGCC	420
CGCGAGTTTC	GCGACCATGC	CGGCCGGCTT	CACCAGATCG	TTGCGGAGAA	ATCCGCTGAA	480
GTTTACTTTG	TCGCGGCCGG	TTTGCCGCTG	AAAATGAAGG	GTTGA		525

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: Amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBP
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Met	Ser	Ser	Leu	Ser	Ala	Gly	Pro	Val	Leu	Val	Leu	Gly	Gly	Ala	Arg
1			5						10					15	
Ser	Gly	Lys	Ser	Ser	Phe	Ser	Glu	Arg	Leu	Val	Glu	Ala	Ser	Gly	Phe
			20					25					30		
Thr	Met	His	Tyr	Val	Ala	Thr	Gly	Arg	Ala	Trp	Asp	Asp	Glu	Met	Arg
			35				40					45			
Glu	Arg	Ile	Asp	His	His	Arg	Thr	Arg	Arg	Gly	Glu	Gly	Trp	Thr	Thr
			50			55					60				
His	Glu	Glu	Pro	Leu	Asp	Leu	Val	Gly	Ile	Leu	Arg	Arg	Ile	Asp	Asp
					70			75					80		
Pro	Ser	His	Val	Val	Leu	Ile	Asp	Cys	Leu	Thr	Leu	Trp	Val	Thr	Asn
				85				90					95		
Leu	Met	Leu	Glu	Glu	Arg	Asp	Met	Thr	Ala	Glu	Phe	Ala	Ala	Leu	Val
			100				105					110			
Ala	Tyr	Leu	Pro	Glu	Ala	Arg	Ala	Arg	Leu	Val	Phe	Val	Ser	Asn	Glu
			115			120				125					
Val	Gly	Leu	Gly	Ile	Val	Pro	Glu	Asn	Arg	Met	Ala	Arg	Glu	Phe	Arg
			130			135				140					
Asp	His	Ala	Gly	Arg	Leu	His	Gln	Ile	Val	Ala	Glu	Lys	Ser	Ala	Glu

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145 150 155 160
Val Tyr Phe Val Ala Gly Leu Pro Leu Lys Met Lys Gly
165 170

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1065 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas denitrificans*
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:
- (ix) FEATURE:
(A) NAME/KEY: cobw
(B) LOCATION: 3892-4956 bp of SEQ ID NO:41
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

ATGACCACTG	CGAGAGCCAA	CCAGGGCAAG	ATCCCGGCGA	CCGTCATCAC	CGGCTTCCTC	60
GGCGCCGGCA	AGACGACGAT	GATCCGCAAC	CTGCTGCAGA	ACGCCGACGG	CAAGCGCATC	120
GGCCTGATCA	TCAACGAGTT	CGGCGATCTT	GGCGTCGACG	GCGATGTCTT	GAAGGGCTGC	180
GGTGCCGAGG	CCTGCACCGA	GGACGACATC	ATCGAGCTCA	CCAATGGCTG	CATCTGCTGC	240
ACCGTGGCTG	ACGATTTTAT	CCCACCACATG	ACGAAGCTGC	TCGAGCGTGA	AAACCGTCCT	300
GACCACATCA	TCATCGAAAC	CTCGGGCCTT	GCCCTGCCGC	AGCCGCTGAT	CGCCGCTTTC	360
AACTGGCCGG	ATATCCGCAG	CGAAGTGACC	GTCGATGGCG	TCGTACCGT	GGTCGACAGC	420
GCCGCCGTTG	CCGCTGGCCG	CTTTGCCGAC	GACCACGACA	AGGTCGATGC	GCTGCGCGTC	480
GAGGACGACA	ATCTCGATCA	CGAAAGCCCG	ATCGAGGAGC	TGTTTCGAGGA	TCAACTGACG	540
GCTGCCGATC	TCATCGTTCT	CAACAAGACC	GATCTGATCG	ATGCCTCCGG	CCTCAAGGCC	600
GTGCGCGACG	AGGTGTCTTC	GCGCACCAGC	CGCAAGCCCA	CGATGATCGA	GGCGAAAAAC	660
GGCGAAGTCG	CCGCTGCCAT	CCTGCTTGGC	CTCGGTGTCG	GCACGGAAAG	CGATATCGCC	720
AACCGCAAGT	CGCATCACGA	GATGGAGCAC	GAGGCAGGTG	AGGAGCACGA	TCACGACGAG	780
TTGACAGCT	TCGTCTGTCG	GCTCGGTTCG	ATCGCCGATC	CGGCCGCCTT	CATCGATCGC	840
CTGAAGGGCG	TAATCGCGGA	GCACGACGTT	CTGCGCCTCA	AGGGTTTTGC	AGACGTGCCC	900
GGCAAGCCGA	TGCGCCTCCT	GATCCAGGCG	GTCGGCGCCC	GCATCGACCA	ATATTACGAC	960
CGCGCCTGGG	GCGCTGGCGA	AAAGCGCGGT	ACGCGCCTCG	TCGTATCGG	CCTGCACGAC	1020
ATGGACGAGG	CGGCGGTGCG	CGCCGCGATC	ACCGCGCTCG	TGTAG		1065

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBW
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Met	Thr	Thr	Ala	Arg	Ala	Asn	Gln	Gly	Lys	Ile	Pro	Ala	Thr	Val	Ile
1				5					10					15	
Thr	Gly	Phe	Leu	Gly	Ala	Gly	Lys	Thr	Thr	Met	Ile	Arg	Asn	Leu	Leu
			20					25					30		
Gln	Asn	Ala	Asp	Gly	Lys	Arg	Ile	Gly	Leu	Ile	Ile	Asn	Glu	Phe	Gly
		35					40					45			
Asp	Leu	Gly	Val	Asp	Gly	Asp	Val	Leu	Lys	Gly	Cys	Gly	Ala	Glu	Ala
	50					55					60				
Cys	Thr	Glu	Asp	Asp	Ile	Ile	Glu	Leu	Thr	Asn	Gly	Cys	Ile	Cys	Cys
65					70					75				80	
Thr	Val	Ala	Asp	Asp	Phe	Ile	Pro	Thr	Met	Thr	Lys	Leu	Leu	Glu	Arg
			85						90					95	
Glu	Asn	Arg	Pro	Asp	His	Ile	Ile	Ile	Glu	Thr	Ser	Gly	Leu	Ala	Leu
			100					105					110		
Pro	Gln	Pro	Leu	Ile	Ala	Ala	Phe	Asn	Trp	Pro	Asp	Ile	Arg	Ser	Glu
		115					120					125			
Val	Thr	Val	Asp	Gly	Val	Val	Thr	Val	Val	Asp	Ser	Ala	Ala	Val	Ala
	130				135						140				
Ala	Gly	Arg	Phe	Ala	Asp	His	Asp	Lys	Val	Asp	Ala	Leu	Arg	Val	
145				150				155						160	
Glu	Asp	Asp	Asn	Leu	Asp	His	Glu	Ser	Pro	Ile	Glu	Glu	Leu	Phe	Glu
			165					170						175	
Asp	Gln	Leu	Thr	Ala	Ala	Asp	Leu	Ile	Val	Leu	Asn	Lys	Thr	Asp	Leu
			180					185					190		
Ile	Asp	Ala	Ser	Gly	Leu	Lys	Ala	Val	Arg	Asp	Glu	Val	Ser	Ser	Arg
	195					200						205			
Thr	Ser	Arg	Lys	Pro	Thr	Met	Ile	Glu	Ala	Lys	Asn	Gly	Glu	Val	Ala
	210					215					220				
Ala	Ala	Ile	Leu	Leu	Gly	Leu	Gly	Val	Gly	Thr	Glu	Ser	Asp	Ile	Ala
225					230					235				240	
Asn	Arg	Lys	Ser	His	Glu	Met	Glu	His	Glu	Ala	Gly	Glu	Glu	His	
			245					250					255		
Asp	His	Asp	Glu	Phe	Asp	Ser	Phe	Val	Val	Glu	Leu	Gly	Ser	Ile	Ala
			260				265					270			
Asp	Pro	Ala	Ala	Phe	Ile	Asp	Arg	Leu	Lys	Gly	Val	Ile	Ala	Glu	His
	275						280					285			
Asp	Val	Leu	Arg	Leu	Lys	Gly	Phe	Ala	Asp	Val	Pro	Gly	Lys	Pro	Met
	290					295					300				

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Arg	Leu	Leu	Ile	Gln	Ala	Val	Gly	Ala	Arg	Ile	Asp	Gln	Tyr	Tyr	Asp
305					310					315					320
Arg	Ala	Trp	Gly	Ala	Gly	Glu	Lys	Arg	Gly	Thr	Arg	Leu	Val	Val	Ile
			325						330					335	
Gly	Leu	His	Asp	Met	Asp	Glu	Ala	Ala	Val	Arg	Ala	Ala	Ile	Thr	Ala
			340						345					350	
Leu	Val														

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3828 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas denitrificans*
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (ix) FEATURE:
 - (A) NAME/KEY: cobN
 - (B) LOCATION: 5060-8887 bp of SEQ ID NO:41
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

ATGCATCTGC	TTCTCGCCCA	GAAAGGAACG	ATCGCCGACG	GCAACGAGGC	GATCGACCTT	60
GGGCAAACGC	CGGCCGATAT	CCTTTTCCTA	TCGGCCGCCG	ACACCGAGCT	CTCCTCGATC	120
GCCGCGGCTC	ACGGCCGACG	CGACGGAGGC	TTGAGCCTGC	GCATCGCCAG	CCTGATGAGC	180
CTGATGCACC	CGATGTCGGT	CGACACTTAC	GTCGAGCGCA	CGGCGCGTCA	CGCCAAGCTG	240
ATCGTCGTCC	GGCCGCTCGG	TGGCGCCAGC	TATTTCCGTT	ATCTGCTGGA	AGCCCTGCAT	300
GCGGCTGCCG	TCACCCATCG	TTTCGAGATC	GCGGTTCTGC	CGGGTGACGA	CAAGCCGGAT	360
CCGGGGCTGG	AGCCTTTCTC	CACCGTCGCA	GCCGACGACC	GCCAGCGCCT	TTGGGCTTAC	420
TTCACCGAAG	GCGGCTCGGA	CAATGCCGGG	CTGTTTCTCG	ACTATGCGGC	CGCACTGGTC	480
ACAGGTGCGG	AGAAGCCGCA	GCCGGCAAAG	CCCCTGTTGA	AGGCCGGCAT	CTGGTGGCCG	540
GGTGCTGGTG	TGATCGGCCG	CAGCGAATGG	CAGTCCCCTG	TTCAGGGACG	GATGGTAGCG	600
AGGGAGGGAT	TCGAACCCCC	GACGGTCGGG	ATCTGCTTTT	ACCGCGCGCT	CGTGCAGAGT	660
GGCGAGACAC	GGCCTGTGGA	GGCGCTGATC	GATGCGCTGG	AGGCTGAAGG	TGTGCGGGCA	720
CTGCCGGTGT	TTGTCTCAAG	CCTCAAGGAT	GCCGTTTCCG	TCGGCACGCT	GCAGGCGATT	780
TTTTCCGAGG	CCGCACCCGA	CGTGGTGATG	AACGCCACTG	GCTTTGCGGT	CTCGTCGCCC	840
GGTGCCGACC	GTCAGCCGAC	GGTGCTGGAA	TCGACCGGTG	CGCCGGTGCT	GCAGGTGATT	900
TTCTCCGGCT	CGTCGCGGGC	GCAATGGGAA	ACGTCGCCGC	AGGGGCTGAT	GGCGCGCGAC	960
CTCGCCATGA	ACGTGGCACT	CCCCGAAGTC	GATGGCGCGA	TCCTTGCGCG	CGCCGTCTCC	1020
TTCAAGGCGG	CGTCGATCTA	TGACGCCAAG	GTGGAGGCCA	ATATCGTCGG	CCATGAGCCG	1080
CTCGAAGGCC	GGGTGCGCTT	TGCCGCTGAT	CTTGCCGTCA	ACTGGGCGAA	CGTGCGCCGG	1140
GCAGAGCCCG	CCGAGCGCCG	TATTGCCATC	GTCATGGCCA	ACTATCCGAA	CCGCGACGGT	1200
CGCCTCGGCA	ACGGTGTCTG	GCTCGACACG	CCGGCCGGTA	CCGTCGAGGT	GCTTAGCGCC	1260
ATGGCGCGGG	AAGGCTATGC	GGTCGGTGAG	GTTCCCGCCG	ATGGCGACGC	GCTGATCCGC	1320
TTTCTGATGG	CCGGGCCGAC	CAATGCGGCG	AGCCATGACC	GTGAAATCCG	CGAGCGTATT	1380

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TCGCTGAACG	ATTACAAAAC	GTTCTTCGAT	TCGCTTCCGA	AACAGATAAA	GGATGAAGTT	1440
GCCGGTCGCT	GGGGCGTGCC	GGAGGCCGAT	GCCTTTTCC	TCGATGGCGC	CTTCGCGCTG	1500
CCGCTCGCCC	GCTTCGGCGA	GGTGATCGTC	GGCATCCAAC	CGGCGCGCGG	CTACAACATC	1560
GATCCGAAGG	AAAGCTACCA	TTCCCCGGAC	CTCGTGCCGC	CGCATGGCTA	TCTCGCCTTC	1620
TACGCCTTCC	TGCGCCAGCA	GTTCGGAGCG	CAGGCGATCG	TCCACATGGG	CAAGCACGGC	1680
AATCTCGAAT	GGCTGCCGGG	CAAGGCGCTG	GCGCTGTCCG	AAACCTGCTA	TCCCCGAAGCG	1740
ATCTTCGGGC	CGCTGCCGCA	CATCTATCCC	TTCATCGTCA	ACGATCCGGG	CGAAGGTACG	1800
CAGGCCAAGC	GCCGCACCAG	CGCCGTATC	ATCGACCACC	TGACCCCGCC	CTTGACGCGC	1860
GCCGAATCCT	ACGGCCCGCT	CAAGGATCTG	GAAGCGCTCG	TCGACGAATA	TTACGACGCC	1920
GCCGGCGGTG	ATCCGCGCCG	CCTCAGGCTG	CTCAGCCGCC	AGATCCTCGA	TCTCGTGCGC	1980
GACATCGGCC	TCGACAGCGA	CGCAGGCATC	GACAGGGGCG	ACAGCGACGA	CAAGGCGCTG	2040
GAAAAGCTCG	ACGCCTATCT	CTGCGACCTC	AAGGAAATGC	AGATCCGCGA	CGGCCTGCAC	2100
ATCTTCGGCG	TTGCGCCGGA	AGGGCGGTTG	TTGACGGACC	TCACCGTAGC	GCTGGCGCGC	2160
GTGCCCCGAG	GTCTCGGCGA	GGGCGGCGAC	CAGAGCCTGC	AGCGGGCGAT	CGCAGCGGAT	2220
GCGGGGCTGC	TGGGGTTTGC	TATTTCCACC	TCGGCGGGGG	GCAACCCCGC	ACGCGACGCC	2280
CAACCCTTCG	ACCCGCTCGA	CTGCGTCATG	TCCGACACCT	GGACAGGCCC	GAAACCGTCC	2340
ATCCTCGCTG	ACCTCTCGGA	CGCCCCCTGG	CGCACCGCCG	GCGATACGGT	CGAGCGCATC	2400
GAGTTGCTTG	CCGCAAATCT	CGTGTCGGGT	GAAGTGGCTT	GCCCCGACCA	CTGGGCCAAC	2460
ACCCGCGCCG	TGCTCGGCGA	AATCGAAACG	CGCCTGAAGC	CGTCGATTTC	AAACTCGGGT	2520
GCCGCCGAGA	TGACCGGCTT	CCTCACCGGT	CTCAGCGGCC	GCTTCGTGCG	CCCCGGTCCA	2580
TCGGGCGCGC	GCCGCGCGG	CCGGCCGGAT	GTGTTGCCGA	CGGGGCGCAA	TTTCTACTCG	2640
GTCGACAGCC	GCGCCGTGCC	GACGCCGGCG	GCTTACGAGC	TTGGCAAGAA	ATCGGCCGAG	2700
CTTCTGATCC	GCCGCTACCT	GCAGGACCAT	GGCGAATGGC	CGTCCTCCTT	TGGCCTGACC	2760
GCCTGGGGCA	CGGCGAACAT	GCGCACCGGC	GGCGACGACA	TCGCCCAGGC	CCTGGCGCTG	2820
ATCGGCGCCA	AGCCACCTG	GGACATGGTC	TCTCGCCGGG	TGATGGGCTA	CGAGATCGTG	2880
CCGCTCGCAG	TCCTCGGCCG	CCCACGCGTC	GACGTGACCT	TGCGCATTTT	CGGCTTCTTC	2940
CGCGATGCCT	TCCCGGACCA	GATCGCGCTC	TTGACAAAGG	CGATCCGCGC	CGTCGCGCTG	3000
GAGGAAGACG	ATGCCGACAA	CATGATCGCC	GCACGCATGC	GGGCGGAAAG	CCGGCGGCTG	3060
GAGGCCGAAG	GCGTGGAAGC	CGCCGAGGCC	GCGCGTCGCG	CCTCCTACCG	CGTCTTTGGC	3120
GCAAAGCCCC	GTGCCTATGG	CGCCGCCCTG	CAGGCGCTGA	TCGACGAGAA	GGGCTGGGAA	3180
ACCAAAGCAG	ATCTCGCCGA	GGCCTATCTT	ACCTGGGGGC	CCTATGCCTA	TGGCGCCGGC	3240
GAGGAGGGCA	AGGCCGAGCG	CGATCTTTTC	GAGGAGCGCC	TGCGCACGAT	AGAGGCGGTG	3300
GTGCAGAACC	AGGACAACCG	CGAGCACGAT	CTGCTCGACA	GCGACGACTA	CTACCACTTC	3360
GAAGGCGGCA	TGAGCGCTGC	CGCCGAACAG	CTCGGCGGTC	ACCGTCCGGC	GATCTACCAC	3420
AACGACCATT	CCCGTCCGGA	AAAGCCTGTG	ATCCGGTCGC	TCGAAGAAGA	GATCGGCCGC	3480
GTGGTCCGGG	CCCGCGTCTG	CAATCCCAAG	TGGATCGATG	GCGTCATGCG	CCACGGATAC	3540
AAGGGCGCCT	TCGAGATCGC	TGCCACGGTC	GACTACATGT	TCGCCTTTGC	CGCGACCACG	3600
GGTGCGGTGC	GCGACCATCA	TTTCGAGGCC	GCTTATCAGG	CGTTTATTGT	CGACGAGCGC	3660
GTGGCTGACT	TCATGCGCGA	CAAGAACCCG	GCCGCCTTTG	CCGAGCTTGC	CGAACGCCTG	3720
CTTGAAGCAA	TCGACCGCAA	TCTCTGGACG	CCGCGCTCGA	ATTCGGCGCG	GTTTGAACCT	3780
GCCGGCATCG	GCACGGCAGC	AACCCGGCTT	CGTGCCGGCA	ATGAATAG		3828

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1275 amino acids
- (B) TYPE: Amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:

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(I) ORGANELLE:

(ix) FEATURE:

(A) NAME/KEY: COBN

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Translation product of SEQ ID NO:48

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Met	His	Leu	Leu	Leu	Ala	Gln	Lys	Gly	Thr	Ile	Ala	Asp	Gly	Asn	Glu
1			5					10					15		
Ala	Ile	Asp	Leu	Gly	Gln	Thr	Pro	Ala	Asp	Ile	Leu	Phe	Leu	Ser	Ala
			20					25					30		
Ala	Asp	Thr	Glu	Leu	Ser	Ser	Ile	Ala	Ala	Ala	His	Gly	Arg	Arg	Asp
			35				40					45			
Gly	Gly	Leu	Ser	Leu	Arg	Ile	Ala	Ser	Leu	Met	Ser	Leu	Met	His	Pro
	50				55					60					
Met	Ser	Val	Asp	Thr	Tyr	Val	Glu	Arg	Thr	Ala	Arg	His	Ala	Lys	Leu
65					70				75					80	
Ile	Val	Val	Arg	Pro	Leu	Gly	Gly	Ala	Ser	Tyr	Phe	Arg	Tyr	Leu	Leu
			85					90					95		
Glu	Ala	Leu	His	Ala	Ala	Ala	Val	Thr	His	Arg	Phe	Glu	Ile	Ala	Val
			100					105					110		
Leu	Pro	Gly	Asp	Asp	Lys	Pro	Asp	Pro	Gly	Leu	Glu	Pro	Phe	Ser	Thr
		115				120					125				
Val	Ala	Ala	Asp	Asp	Arg	Gln	Arg	Leu	Trp	Ala	Tyr	Phe	Thr	Glu	Gly
	130				135					140					
Gly	Ser	Asp	Asn	Ala	Gly	Leu	Phe	Leu	Asp	Tyr	Ala	Ala	Ala	Leu	Val
145					150				155					160	
Thr	Gly	Ala	Glu	Lys	Pro	Gln	Pro	Ala	Lys	Pro	Leu	Leu	Lys	Ala	Gly
			165					170					175		
Ile	Trp	Trp	Pro	Gly	Ala	Gly	Val	Ile	Gly	Val	Ser	Glu	Trp	Gln	Ser
			180					185					190		
Leu	Val	Gln	Gly	Arg	Met	Val	Ala	Arg	Glu	Gly	Phe	Glu	Pro	Pro	Thr
		195				200						205			
Val	Gly	Ile	Cys	Phe	Tyr	Arg	Ala	Leu	Val	Gln	Ser	Gly	Glu	Thr	Arg
	210					215					220				
Pro	Val	Glu	Ala	Leu	Ile	Asp	Ala	Leu	Glu	Ala	Glu	Gly	Val	Arg	Ala
225					230				235					240	
Leu	Pro	Val	Phe	Val	Ser	Ser	Leu	Lys	Asp	Ala	Val	Ser	Val	Gly	Thr
			245					250						255	
Leu	Gln	Ala	Ile	Phe	Ser	Glu	Ala	Ala	Pro	Asp	Val	Val	Met	Asn	Ala
			260					265					270		
Thr	Gly	Phe	Ala	Val	Ser	Ser	Pro	Gly	Ala	Asp	Arg	Gln	Pro	Thr	Val
		275					280					285			
Leu	Glu	Ser	Thr	Gly	Ala	Pro	Val	Leu	Gln	Val	Ile	Phe	Ser	Gly	Ser
	290					295					300				
Ser	Arg	Ala	Gln	Trp	Glu	Thr	Ser	Pro	Gln	Gly	Leu	Met	Ala	Arg	Asp
305					310					315				320	
Leu	Ala	Met	Asn	Val	Ala	Leu	Pro	Glu	Val	Asp	Gly	Arg	Ile	Leu	Ala
			325					330						335	
Arg	Ala	Val	Ser	Phe	Lys	Ala	Ala	Ser	Ile	Tyr	Asp	Ala	Lys	Val	Glu
			340					345					350		
Ala	Asn	Ile	Val	Gly	His	Glu	Pro	Leu	Glu	Gly	Arg	Val	Arg	Phe	Ala
		355					360					365			
Ala	Asp	Leu	Ala	Val	Asn	Trp	Ala	Asn	Val	Arg	Arg	Ala	Glu	Pro	Ala
	370					375					380				
Glu	Arg	Arg	Ile	Ala	Ile	Val	Met	Ala	Asn	Tyr	Pro	Asn	Arg	Asp	Gly
385					390					395				400	
Arg	Leu	Gly	Asn	Gly	Val	Gly	Leu	Asp	Thr	Pro	Ala	Gly	Thr	Val	Glu

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Val	Leu	Ser	Ala	405	Ala	Arg	Glu	Gly	410	Tyr	Ala	Val	Gly	Glu	415	Pro
Ala	Asp	Gly	420	Ala	Leu	Ile	Arg	Phe	425	Leu	Met	Ala	Gly	430	Pro	Thr
Ala	Ala	435	Ser	His	Asp	Arg	Glu	Ile	440	Arg	Glu	Arg	Ile	445	Ser	Leu
Tyr	450	Lys	Thr	Phe	Phe	455	Asp	Ser	460	Leu	Pro	Lys	Gln	465	Ile	Lys
465	Ala	Gly	Arg	Trp	Gly	470	Val	Pro	475	Glu	Ala	Asp	Pro	480	Phe	Phe
Ala	Phe	Ala	Leu	Pro	Leu	Ala	Arg	Phe	485	Gly	Glu	Val	Ile	490	Val	Gly
Gln	Pro	Ala	Arg	Gly	Tyr	Asn	Ile	500	505	Asp	Pro	Lys	Glu	510	Ser	Tyr
Pro	Asp	Leu	Val	Pro	Pro	His	Gly	515	520	Tyr	Leu	Ala	Phe	525	Tyr	Ala
Arg	Gln	Gln	Phe	Gly	Ala	Gln	Ala	530	535	Ile	Val	His	Met	540	Gly	Lys
Asn	Leu	Glu	Trp	Leu	Pro	Gly	Lys	545	550	Ala	Leu	Ala	Leu	555	Ser	Glu
Tyr	Pro	Glu	Ala	Ile	Phe	Gly	Pro	560	565	Leu	Pro	His	Ile	570	Tyr	Pro
Val	Asn	Asp	Pro	Gly	Glu	Gly	Thr	575	580	Gln	Ala	Lys	Arg	585	Arg	Thr
Val	Ile	610	Ile	Asp	His	Leu	Thr	600	605	Pro	Pro	Leu	Thr	610	Ala	Glu
Gly	Pro	Leu	Lys	Asp	Leu	Glu	Ala	615	620	Leu	Val	Asp	Glu	625	Tyr	Tyr
Ala	Gly	Gly	Asp	Pro	Arg	Arg	Leu	630	635	Arg	Leu	Leu	Ser	640	Arg	Gln
Asp	Leu	Val	Arg	645	Ile	Gly	Leu	645	650	Asp	Ser	Asp	Ala	655	Gly	Ile
Gly	Asp	Ser	Asp	660	Lys	Ala	Leu	665	670	Glu	Lys	Leu	Asp	675	Ala	Tyr
Asp	Leu	Lys	Glu	680	Met	Gln	Ile	685	690	Arg	Asp	Gly	Leu	695	His	Ile
Ala	Pro	Glu	Gly	700	Arg	Leu	Thr	705	710	Asp	Leu	Thr	Val	715	Ala	Leu
Val	Pro	Arg	Gly	720	Leu	Gly	Glu	725	730	Gly	Gly	Asp	Gln	735	Ser	Leu
Ile	Ala	Ala	Asp	740	Ala	Gly	Leu	745	750	Phe	Ala	Ile	Pro	755	Thr	Ser
Gly	Gly	Asn	Pro	755	Ala	Arg	Asp	760	765	Gln	Pro	Phe	Asp	770	Pro	Leu
Val	Met	Ser	Asp	775	Thr	Trp	Thr	780	785	Gly	Pro	Lys	Pro	790	Ser	Ile
Leu	Ser	Asp	Ala	790	Pro	Trp	Arg	795	800	Ala	Gly	Asp	Thr	805	Val	Glu
Glu	Leu	Leu	Ala	805	Asn	Leu	Val	810	815	Gly	Glu	Leu	Ala	820	Cys	Pro
His	Trp	Ala	Asn	820	Thr	Arg	Ala	825	830	Leu	Gly	Glu	Ile	835	Thr	Arg
Lys	Pro	Ser	Ile	835	Ser	Asn	Ser	840	845	Gly	Ala	Ala	Glu	850	Met	Thr
Thr	Gly	Leu	Ser	850	Gly	Arg	Phe	855	860	Val	Ala	Pro	Gly	865	Pro	Ser
Thr	Arg	Gly	Arg	865	Pro	Asp	Val	870	875	Leu	Pro	Thr	Gly	880	Arg	Asn
Val	Asp	Ser	Arg	885	Ala	Val	Pro	890	895	Ala	Ala	Tyr	Glu	900	Leu	Gly
Lys	Ser	Ala	Glu	900	Leu	Leu	Ile	905	910	Arg	Arg	Tyr	Leu	915	Gln	Asp

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Trp	Pro	Ser	900	Ser	Phe	Gly	Leu	Thr	905	Ala	Trp	Gly	Thr	910	Ala	Asn	Met	Arg
Thr	Gly	Gly	915	Asp	Asp	Ile	Ala	Gln	920	Ala	Leu	Ala	Leu	925	Ile	Gly	Ala	Lys
Pro	Thr	Trp	930	Asp	Met	Val	Ser	Arg	935	Arg	Val	Met	Gly	940	Tyr	Glu	Ile	Val
945	Pro	Leu	Ala	Val	950	Gly	Arg	Pro	955	Arg	Val	Asp	Val	960	Thr	Leu	Arg	Ile
Ser	Gly	Phe	965	Phe	Arg	Asp	Ala	Phe	970	Pro	Asp	Gln	Ile	975	Ala	Leu	Phe	Asp
Lys	Ala	Ile	980	Arg	Ala	Val	Ala	Leu	985	Glu	Glu	Asp	Asp	990	Ala	Asp	Asn	Met
Ile	Ala	Ala	995	Arg	Met	Arg	Ala	Glu	1000	Ser	Arg	Arg	Leu	1005	Glu	Ala	Glu	Gly
1010	Val	Glu	Ala	Ala	Glu	Ala	Ala	Arg	1015	Arg	Ala	Ser	Tyr	1020	Arg	Val	Phe	Gly
1025	Ala	Lys	Pro	Gly	1030	Ala	Tyr	Gly	1035	Ala	Ala	Leu	Gln	1040	Ala	Leu	Ile	Asp
Lys	Gly	Trp	1045	Glu	1050	Thr	Lys	Ala	1055	Asp	Leu	Ala	Glu	1060	Ala	Tyr	Leu	Thr
Gly	Ala	Tyr	1065	Ala	1070	Tyr	Gly	Ala	1075	Gly	Glu	Glu	Gly	1080	Lys	Ala	Glu	Arg
Leu	Phe	Glu	1085	Glu	1090	Arg	Leu	Arg	1095	Thr	Ile	Glu	Ala	1100	Val	Val	Gln	Asn
1105	Asp	Asn	Arg	Glu	1110	His	Asp	Leu	1115	Leu	Asp	Ser	Asp	1120	Asp	Tyr	Tyr	Gln
Glu	Gly	Gly	1125	Met	1130	Ser	Ala	Ala	1135	Ala	Glu	Gln	Leu	1140	Gly	Gly	His	Arg
Ala	Ile	Tyr	1145	His	1150	Asn	Asp	His	1155	Ser	Arg	Pro	Glu	1160	Lys	Pro	Val	Ile
Ser	Leu	Glu	1165	Glu	1170	Glu	Ile	Gly	1175	Arg	Val	Val	Arg	1180	Ala	Arg	Val	Val
Pro	Lys	Trp	1185	Ile	1190	Asp	Gly	Val	1195	Met	Arg	His	Gly	1200	Tyr	Lys	Gly	Ala
Glu	Ile	Ala	1205	Ala	1210	Thr	Val	Asp	1215	Tyr	Met	Phe	Ala	1220	Phe	Ala	Ala	Thr
1225	Gly	Ala	Val	Arg	1230	Asp	His	His	1235	Phe	Glu	Ala	Ala	1240	Tyr	Gln	Ala	Phe
Val	Asp	Glu	1245	Arg	1250	Val	Ala	Asp	1255	Phe	Met	Arg	Asp	1260	Lys	Asn	Pro	Ala
Phe	Ala	Glu	1265	Leu	1270	Ala	Glu	Arg	1275	Leu	Leu	Glu	Ala	1280	Ile	Asp	Arg	Asn
Trp	Thr	Pro	1285	Arg	1290	Ser	Asn	Ser	1295	Ala	Arg	Phe	Glu	1300	Leu	Ala	Gly	Ile
Thr	Ala	Ala	1305	Thr	1310	Arg	Leu	Arg	1315	Ala	Gly	Asn	Glu	1320	Ala	Gly	Ile	Gly

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 645 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas denitrificans*

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- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: cobo
- (B) LOCATION: 9034-9678 bp of SEQ ID NO:41
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

ATGAGCGACG	AGACGACAGT	AGGCGGCGAA	GCCCCGGCCG	AGAAGGACGA	TGCCCCGCCAC	60
GCCATGAAGA	TGGCGAAGAA	GAAGGCAGCA	CGCGAAAAGA	TCATGGCGAC	GAAGACCGAC	120
GAGAAGGGTC	TGATCATCGT	CAACACCGGC	AAAGGCAAGG	GCAAGTCGAC	CGCCGGCTTC	180
GGCATGATCT	TCCGCCATAT	CGCCCACGGC	ATGCCCTGCG	CCGTCGTGCA	GTTCATCAAG	240
GGTGCGATGG	CAACCGGCGA	GCGCGAGTTG	ATCGAGAAGC	ATTTTCGGCGA	TGTCTGCCAG	300
TTCTACACGC	TGGGCGAGGG	CTTCACCTGG	GAAACGCAGG	ATCGCGCCCCG	CGATGTTGCG	360
ATGGCTGAAA	AGGCCTGGGA	GAAGGCGAAG	GAAGTATGCC	GTGACGAGCG	CAACTCGATG	420
GTGCTGCTCG	ACGAGATCAA	CATTGCTCTG	CGCTACGACT	ACATCGACGT	CGCCGAAGTG	480
GTGCGCTTCC	TGAAGGAAGA	AAAGCCGCAC	ATGACGCATG	TGGTGCTCAC	CGGCCGCAAC	540
GCGAAAGAAG	ACCTGATCGA	AGTCGCCGAT	CTCGTCACTG	AGATGGAGCT	GATCAAGCAT	600
CCGTTCCGTT	CCGGCATCAA	GGCGCAGCAG	GGCGTGGAGT	TCTGA		645

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acid
- (B) TYPE: Amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: Pseudomonas denitrificans
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBO
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO: 50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Met Ser Asp Glu Thr Thr Val Gly Gly Glu Ala Pro Ala Glu Lys Asp

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1	5	10	15												
Asp	Ala	Arg	His	Ala	Met	Lys	Met	Ala	Lys	Lys	Lys	Ala	Ala	Arg	Glu
	20							25				30			
Lys	Ile	Met	Ala	Thr	Lys	Thr	Asp	Glu	Lys	Gly	Leu	Ile	Ile	Val	Asn
	35						40					45			
Thr	Gly	Lys	Gly	Lys	Gly	Lys	Ser	Thr	Ala	Gly	Phe	Gly	Met	Ile	Phe
	50					55					60				
Arg	His	Ile	Ala	His	Gly	Met	Pro	Cys	Ala	Val	Val	Gln	Phe	Ile	Lys
	65				70					75				80	
Gly	Ala	Met	Ala	Thr	Gly	Glu	Arg	Glu	Leu	Ile	Glu	Lys	His	Phe	Gly
			85					90					95		
Asp	Val	Cys	Gln	Phe	Tyr	Thr	Leu	Gly	Glu	Gly	Phe	Thr	Trp	Glu	Thr
			100					105					110		
Gln	Asp	Arg	Ala	Arg	Asp	Val	Ala	Met	Ala	Glu	Lys	Ala	Trp	Glu	Lys
		115					120					125			
Ala	Lys	Glu	Leu	Ile	Arg	Asp	Glu	Arg	Asn	Ser	Met	Val	Leu	Leu	Asp
	130					135					140				
Glu	Ile	Asn	Ile	Ala	Leu	Arg	Tyr	Asp	Tyr	Ile	Asp	Val	Ala	Glu	Val
	145				150					155				160	
Val	Arg	Phe	Leu	Lys	Glu	Glu	Lys	Pro	His	Met	Thr	His	Val	Val	Leu
			165					170					175		
Thr	Gly	Arg	Asn	Ala	Lys	Glu	Asp	Leu	Ile	Glu	Val	Ala	Asp	Leu	Val
			180					185					190		
Thr	Glu	Met	Glu	Leu	Ile	Lys	His	Pro	Phe	Arg	Ser	Gly	Ile	Lys	Ala
		195					200					205			
Gln	Gln	Gly	Val	Glu	Phe										
	210														

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 955 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: Methanobacterium ivanovii
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: containing corA or sumT gene
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Nucleotide sequence of the 5' to 3' strand from the 955 bp fragment of Methanobacterium ivanovii

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

CCATAATTCT TTTATAATTT AAACGGTGAA CACATGGTAG TTTATTTAGT AGGTGCGGGT

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CCAGGAGATC	CCGAACCTTAT	CACTCTCAAA	GCTGTAAACG	TGTTAAAAAA	AGCGGATGTT	120
GTACTGTACG	ACAAACCTGC	AAATGAAGAA	ATTTTAAAGT	ATGCTGAAGG	TGCAAAACTA	180
ATATATGTCG	GAAAACAAGC	AGGACATCAT	TACAAATCTC	AAAATGAAAT	CAATACTCTT	240
CTTGTTGAAG	AAGCAAAAGA	AAATGATTTA	GTAGTACGCC	TAAAGGTGG	AGACCCCTTT	300
GTATTTGGAA	GAGGAGGCGA	GGAAATTCTG	GCCCTTG TAG	AAGAAGGAAT	TGATTTTGAG	360
TTAGTTCCAG	GGGTAACCTC	TGCAATTGGA	GTTCCAACAA	CAATTGGGCT	TCCAGTTACT	420
CATAGAGGTG	TTGCAACATC	GTTTACAGTT	GTTACAGGTC	ATGAAGACCC	AACAAAATGC	480
AAGAAACAGG	TAGGATGGGA	CTTTAAAGCA	GATACTATTG	TAATACTTAT	GGGTATTGGA	540
AATTTAGCTG	AAAATACAGC	AGAAATTATG	AAACATAAAG	ATCCTGAAAC	TCCAGTTTGT	600
GTAATTGAAA	ATGGTACGAT	GGAAGGTCAA	AGGATAATAA	CGGGCACACT	GGAAAATATA	660
GCTGGAAAGG	ATATTAAACC	TCCTGCTTTA	GTGGTATTGG	AAATGTTGTC	AATGTTTTTA	720
AAGAAATGAA	TCAAATCAGT	GGCTGATCTA	TTAAGAAGGC	AATATCATGA	ATGGATTAGA	780
AGGTAAAAAA	ATTGTTATAA	CAAGACCTGC	TGAAAGGGCT	AAAGACTCAG	TTGAAATGGT	840
AAAATCTTAT	GGAGCAGTTC	CAATTGTAAC	TCCTACAATT	GAAC TCAAAG	ATTCCAAGCC	900
AGAAGAAGTG	ATAAAATTAT	GTAATATGAT	AAATGAACCT	TGATTGGCCT	TATAT	955

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 696 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

(A) ORGANISM: *Methanobacterium ivanovii*

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(ix) FEATURE:

(A) NAME/KEY: corA or sumT

(B) LOCATION: 34-729 bp of SEQ ID NO:52

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ATGGTAGTTT	ATTTAGTAGG	TGCGGGTCCA	GGAGATCCCG	AACTTATCAC	TCTCAAAGCT	60
GTAAACGTGT	TAAAAAAAGC	GGATGTTGTA	CTGTACGACA	AACCTGCAAA	TGAAGAAATT	120
TTAAAGTATG	CTGAAGGTGC	AAAAC TAATA	TATGTCGGAA	AACAAGCAGG	ACATCATTAC	180
AAATCTCAAA	ATGAAATCAA	TACTCTTCTT	GTTGAAGAAG	CAAAAGAAAA	TGATTTAGTA	240
GTACGCCTTA	AAGGTGGAGA	CCCCTTTGTA	TTTGGAAGAG	GAGGCGAGGA	AATTCTGGCC	300
CTTG TAGAAG	AAGGAATTGA	TTTTGAGTTA	GTTCCAGGGG	TAAC TTCTGC	AATTGGAGTT	360
CCAACAACAA	TTGGGCTTCC	AGTTACTCAT	AGAGGTGTTG	CAACATCGTT	TACAGTTGTT	420
ACAGGTCATG	AAGACCCAAC	AAAATGCAAG	AAACAGGTAG	GATGGGACTT	TAAAGCAGAT	480
ACTATTGTAA	TACTTATGGG	TATTGGAAAT	TTAGCTGAAA	ATACAGCAGA	AATTATGAAA	540
CATAAAGATC	CTGAAACTCC	AGTTTGTGTA	ATTGAAAATG	GTACGATGGA	AGGTCAAAGG	600
ATAATAACGG	GCACACTGGA	AAATATAGCT	GGAAAGGATA	TTAAACCTCC	TGCTTTAGTG	660
GTATTGGAAG	TGTTGTCAAT	GTTTTTAAAG	AAATGA			696

(2) INFORMATION FOR SEQ ID NO: 54:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
(A) ORGANISM: Methanobacterium ivanovii
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:
- (ix) FEATURE:
(A) NAME/KEY: CORA
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Translation product of SEQ ID NO:53
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Met Val Val Tyr Leu Val Gly Ala Gly Pro Gly Asp Pro Glu Leu Ile
1 5 10 15
Thr Leu Lys Ala Val Asn Val Leu Lys Lys Ala Asp Val Val Leu Tyr
20 25 30
Asp Lys Pro Ala Asn Glu Glu Ile Leu Lys Tyr Ala Glu Gly Ala Lys
35 40 45
Leu Ile Tyr Val Gly Lys Gln Ala Gly His His Tyr Lys Ser Gln Asn
50 55 60
Glu Ile Asn Thr Leu Leu Val Glu Glu Ala Lys Glu Asn Asp Leu Val
65 70 75 80
Val Arg Leu Lys Gly Gly Asp Pro Phe Val Phe Gly Arg Gly Gly Glu
85 90 95
Glu Ile Leu Ala Leu Val Glu Glu Gly Ile Asp Phe Glu Leu Val Pro
100 105 110
Gly Val Thr Ser Ala Ile Gly Val Pro Thr Thr Ile Gly Leu Pro Val
115 120 125
Thr His Arg Gly Val Ala Thr Ser Phe Thr Val Val Thr Gly His Glu
130 135 140
Asp Pro Thr Lys Cys Lys Lys Gln Val Gly Trp Asp Phe Lys Ala Asp
145 150 155 160
Thr Ile Val Ile Leu Met Gly Ile Gly Asn Leu Ala Glu Asn Thr Ala
165 170 175
Glu Ile Met Lys His Lys Asp Pro Glu Thr Pro Val Cys Val Ile Glu
180 185 190
Asn Gly Thr Met Glu Gly Gln Arg Ile Ile Thr Gly Thr Leu Glu Asn
195 200 205
Ile Ala Gly Lys Asp Ile Lys Pro Pro Ala Leu Val Val Leu Glu Met
210 215 220
Leu Ser Met Phe Leu Lys Lys
225 230

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(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: polypeptide

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: E. coli
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: fragment of cysG protein
- (B) LOCATION: amino acids 204-460
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

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Glu Gln Leu Ile Asn Glu Pro Leu Asp His Arg Gly Glu Val Val Leu
      5      10      15
Val Gly Ala Gly Pro Gly Asp Ala Gly Leu Leu Thr Leu Lys Gly Leu
      20      25      30
Gln Gln Ile Gln Gln Ala Asp Val Val Tyr Asp Arg Leu Val Ser
      35      40      45
Asp Asp Ile Met Asn Leu Val Arg Arg Asp Ala Asp Arg Val Phe Val
      50      55      60
Gly Lys Arg Ala Gly Tyr His Cys Val Pro Gln Glu Glu Ile Asn Gln
      65      70      75      80
Ile Leu Leu Arg Glu Ala Gln Lys Gly Lys Arg Val Val Arg Leu Lys
      85      90      95
Gly Gly Asp Pro Phe Ile Phe Gly Arg Gly Gly Glu Glu Leu Glu Thr
      100      105      110
Leu Cys Asn Ala Gly Ile Pro Phe Ser Val Val Pro Gly Ile Thr Ala
      115      120      125
Ala Ser Gly Cys Ser Ala Tyr Ser Gly Ile Pro Leu Thr His Arg Asp
      130      135      140
Tyr Ala Gln Ser Val Arg Leu Ile Thr Gly His Leu Lys Thr Gly Gly
      145      150      155      160
Glu Leu Asp Trp Glu Asn Leu Ala Ala Glu Lys Gln Thr Leu Val Phe
      165      170      175
Tyr Met Gly Leu Asn Gln Ala Ala Thr Ile Gln Gln Lys Leu Ile Glu
      180      185      190
His Gly Met Pro Gly Glu Met Pro Val Ala Ile Val Glu Asn Gly Thr
      195      200      205
Ala Val Thr Gln Arg Val Ile Asp Gly Thr Leu Thr Gln Leu Gly Glu
      210      215      220
Leu Ala Gln Gln Met Asn Ser Pro Ser Leu Ile Ile Gly Arg Val
      225      230      235      240
Val Gly Leu Arg Asp Lys Leu Asn Trp Phe Ser

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245 250

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
 - (A) NAME/KEY: fragment of sumT gene
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

CGCGGAATTC CCNGGNGAYC CNGARCT

27

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
 - (A) NAME/KEY: fragment of sumT gene
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CGCGGAATTC GTRTAYCTWG TDGGWGC

27

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
 - (A) NAME/KEY: fragment of sumT gene
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CGCGAAGCTT RTTYTCWAGD GTNCC

25

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: oligonucleotide

(ix) FEATURE:

- (A) NAME/KEY: fragment of sumT gene
- (B) LOCATION: -12 - 15
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: as seen in specification, p. 182,

line 5.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GGCCGAATTC ATATGGTAGT TTATTTA

27

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: oligonucleotide

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: As seen in specification on p. 182,

line 10. Hybrid fragment complementary strand derived from sumT gene sequence.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GGCCGAGCTC TATTACATAA TT

220